

THESIS

PARASITE COMMUNITIES OF WILD TURKEYS (*MELEAGRIS GALLOPAVO*) IN
COLORADO

Submitted by

Paige Willever Shilling Littman

Department of Biology

In partial fulfillment of the requirements

For the Degree of Master of Science

Colorado State University

Fort Collins, Colorado

Fall 2014

Master's Committee:

Advisor: Janice Moore

Cameron Ghalambor
Kristy Pabilonia

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ABSTRACT

PARASITE COMMUNITIES OF WILD TURKEYS (*MELEAGRIS GALLOPAVO*) IN COLORADO

Wild turkeys (*Meleagris gallopavo*) are the largest of the galliform birds, are commonly hunted birds, and they are non-migratory. Wild turkeys were originally found over most of the United States. In the early 1900s they experienced widespread population declines which are thought to have been caused by overhunting and habitat loss. Due to many reintroduction efforts, the wild turkey is now found in its historical range and it has expanded its range even further. However, considering the popularity of wild turkeys as game birds, relatively few studies have addressed their parasites, and specifically the helminth parasites.

Island Biogeography Theory has been applied to parasite and host relationships in which the host is considered an island. In particular, the Island Size hypothesis predicts that a larger island will allow for greater species diversity due to the increased area, and by extension, larger host species, in terms of body mass, will have more species of parasites. This study evaluates whether or not galliform birds support the Island Size Hypothesis in terms of their parasite communities. Birds in the order Galliformes have a wide range of sizes and are generally non-migratory; thus they will not pick up parasites from different locations. I reviewed twenty six studies of 19 species of galliform birds and recorded the number of helminth species reported in each host bird species. Based on these data, I show that there is a positive correlation ($R^2 = 0.212$) between galliform host size and number of helminth parasite species. The model that best fits the data includes both the mean mass of the host species as well as the family of the host species.

This is the first survey of helminth parasites in wild turkeys of Colorado. I collected 24 wild turkey intestines that were donated by hunters. These intestines were examined for helminth parasites, which were collected and identified. A total of 7 different species of helminth parasites were identified in these Colorado wild turkeys. Cestodes were the most commonly identified helminths, followed by acanthocephalans, trematodes, and nematodes.

The Colorado data were then compared to a previous study of the helminths of wild turkeys in both Florida and New Zealand. A total of 14 helminth parasite species were reported from wild turkeys in Florida while 6 helminth species were reported in wild turkeys from New Zealand. These data suggest that there are differences in these parasite communities in terms of parasite species richness and prevalence of each helminth species.

The fact that wild turkeys are not only a popular game bird, but also a common component of domestic poultry operations underscored the importance of understanding their parasites. This knowledge can help us to harvest wild turkeys safely when hunting as well as minimize the transfer of parasites between domestic and wild turkeys.

ACKNOWLEDGEMENTS

There are numerous people without whom this thesis would not have been possible without. First and foremost I thank Dr. Janice Moore. Dr. Moore provided immeasurable support and guidance, including attending a NWTB banquet with me before I had even officially started graduate school. My committee members, Dr. Cameron Ghalambor and his vast knowledge of ecology and Dr. Kristy Pabilonia and her expertise on avian diseases, provided valuable insight and help. Dr. Lora Ballweber helped me to identify some cestodes and without her help, I would have been lost.

Ashley Janich spent an immeasurable amount of hours digging through turkey intestines with me, and for that I will be forever grateful. Without her, I would likely still be extracting parasites from the intestines.

There are a few teachers who have had a huge influence on my life. First, Mr. Kendall was my science teacher in junior high. During his class, I discovered my passion for biology and have held that passion close ever since. More recently, Dr. Valerie McKenzie was my parasitology professor at the University of Colorado and without her passion for parasites, I never would have entered the field myself.

My wonderful husband, Christopher Littman, has been supportive throughout my graduate career and put up with venturing out to find turkey hunters, vials of parasites on the kitchen table, and turkey intestines in the freezer. If that isn't true love, then I don't know what is. My parents, Susan Shilling and Charles Shilling, and my sister, Lizzy Shilling, have always supported me as far back as I can remember and they continue to do so.

I would also like to thank the Biology Department for giving me the opportunity to be a Graduate Teaching Assistant, and I would especially like to thank the laboratory coordinator,

Donna Weedman. She has allowed me the opportunity to grow as a teacher and has shown me how rewarding teaching can be.

My lab mates, Charles Stone and Skyler Griffin, have been instrumental in my success. I truly appreciate all of their advice, suggestions, and encouragement. Charles even drove with me once to meet a turkey hunter to make sure that I did not get kidnapped in the process of trying to collect my samples.

Numerous turkey hunters made my research possible including Russ Means, Ryan Urie, Tom Haverty, Linus Leppink, Keith Ewald, Ed Gorman, Broox Boze, Dawson Swanson, Jeff Mekeldore, and Joe Cugliat. I cannot thank them enough for making the extra effort to save their turkey intestines for me.

Lastly, I thank the turkeys and their parasites, and all of the people who look at me like I am crazy when I tell them what I am studying – those looks always help to remind me just how much I love it.

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CHAPTER 1: Literature Review

Several broad ecological concepts can be applied to the study of the parasites of wild turkeys (*Meleagris gallopavo*). One of these concepts is Island Biogeography Theory and the Island Size Hypothesis, in this case where hosts are analogous to islands. Additionally, invasion biology can be applied to the parasites of wild turkeys because the parasites of introduced hosts are establishing in new areas. After introducing some concepts of parasite community ecology, I will additionally review Island Biogeography Theory, the Island Size Hypothesis, and invasion biology. This chapter will conclude with an introduction to wild turkeys, their biology, history, and parasites.

Parasite Communities

Historically, ecologists paid little attention to parasites when considering community ecology studies (Poulin, 1995; Moore, 2012). Holmes was among the first to study parasites as a community in the early 1960s when he examined the concurrent infections of *Hymenolepis diminuta* and *Moniliformis dubius* in a rat host (Holmes, 1961; Holmes, 1962; Poulin, 1995). Since then, the study of parasite communities has expanded. For instance, intestinal parasite communities are an ideal way to study ecosystems because communities can be replicated by studying multiple intestines, the community boundary is clear, and the location within the intestine can yield information about relative resource use (Moore and Simberloff, 1990; Poulin, 1995).

Parasite communities can be examined on several different levels. Possibly the most common is the infracommunity level. An infracommunity consists of all the parasites species in one host (Bush et al., 1997). Individual hosts can have variation in infracommunity richness due to individual host size, diet, habitat, population size, and host species (Poulin, 1995). Another

level of parasite community is the component community which is composed of all of the infracommunities in a host population (Bush et al., 1997). There can also be variation in the component communities due to ecological factors (Poulin, 1995). In this chapter, I will examine the Theory of Island Biogeography and the Island Size Hypothesis as they relate to parasite communities, parasites in introduced or reintroduced hosts, wild turkey history and biology, and the parasites of wild turkeys.

The Theory of Island Biogeography and Island Size Hypothesis

History of the Theory of Island Biogeography: A Brief Review

The Theory of Island Biogeography was originally a way to examine the factors that affect species richness on islands (MacArthur and Wilson, 1967). Biogeography is the study of how diversity is distributed and MacArthur and Wilson applied this to islands because they represent unique ecosystems (Reperant, 2010). They proposed that an island will reach equilibrium in terms of species richness when the immigration rates and extinction rates are equal. The number of species on an island at this equilibrium point would depend on characteristics of the island such as distance from the mainland, island size, and resources (Reperant, 2010). The theory has since been applied to isolated communities, such as mountains and fragmented areas, which can also be considered habitat islands.

The Theory of Island Biogeography has been further expanded to include parasite hosts as islands. Janzen was one of the first researchers to suggest this application for the Theory of Island Biogeography by applying it to insects and their host plants (Janzen, 1968; Janzen, 1973; Kuris et al., 1980). A host may reach an equilibrium number of parasite species and this equilibrium may be based on island-like characteristics such as distance to other hosts and host size. Parasites can colonize hosts and also become extinct in hosts, just as species can colonize

and become extinct on islands (Reperant, 2010). Additionally, evolution can play a role in terms of the co-evolutionary arms race between hosts and parasites, which could lead to speciation or extinction.

Examining parasite biodiversity is an important aspect of ecology because parasites make up a large percentage of overall biodiversity. Studying the factors that affect parasite biodiversity is essential to understanding disease and conservation (Kamiya et al., 2013). For this reason, the factors influencing parasite diversity have been widely studied; however the factors that drive parasite diversity are still not well understood due to the complexity of parasite-host interactions (Freeland, 1979; Kuris et al. 1980; Moore et al., 1988; Guegan et al., 1992; Gregory, 1996; Morand and Poulin, 1998; Lindenfors et al., 2007; Kamiya et al., 2013; Patterson and Ruckstuhl, 2013).

Levels at Which Hosts Can Be Considered Islands

There are various levels at which hosts can be considered islands. First, the individual host can be an island. If an individual host is an island, the parasite infracommunity, or all of the parasite species within the host will be equal to the parasite species richness. An individual host as an island is an appropriate way to study the Theory of Island Biogeography because the host has a discrete boundary (Kuris et al., 1980). New species are introduced to the island when the host becomes infected. Extinction occurs when the parasite either dies or leaves the host (Kuris et al., 1980). Also, there may be competitive or facilitative interactions much like those on an actual island, and the immune response can be analogous to a predator (Kuris et al., 1980).

Second, host populations can be islands to the parasite component community. Many parasites are transmitted by close contact or through fecal contamination and therefore these parasites are shared within a host population or social group (Freeland, 1979). Studies examining

host populations as islands are rare as normally populations do not have discrete boundaries (Kuris et al., 1980). Primate social groups are an example of how host populations can be islands as members of the group interact frequently, but they rarely interact with other groups. One study of primate social groups found that within a group, every individual had the same number of species of intestinal protozoan parasites (Freeland, 1979). For three of the four species of primates studied, there were intergroup differences in the species of intestinal protozoan parasites (Freeland, 1979). There is probably very little transmission between different social groups because most of the parasites are transmitted through fecal material, which in the case of a social group that defends its space, limits exposure to the space occupied by that group. This is supported by the fact that the number of protozoan species found in the single primate social groups was less than the number of species found throughout the entire primate population (Freeland, 1979). Freeland also found that there was a positive correlation between primate social group size and the number of protozoan species (Freeland, 1979). Another example of the relationships between group size and parasite intensity can be seen in bobwhite quail. Parasite intensity of *Trichostrongylus tenuis* was higher for bobwhite quails in large coveys than small coveys ($P=0.06$). *T. tenuis* is directly transmitted, and therefore this parasite may reflect group size more directly than other parasites that have intermediate hosts due to the variations in time and space that are introduced by intermediate hosts (Moore et al., 1988).

Finally, host species and the entire geographic range that the species covers can be considered an island. An entire host species represents the entire habitable area for a parasite. However, collecting data at this level would be not only extremely difficult, if not impossible, because it would necessitate a complete parasite census for the entire host species (Kuris et al.,

1980). The vast majority of species in the world have not yet been studied that thoroughly. I will therefore focus on individual hosts as islands.

Individual Hosts as Islands

There are many factors that can affect the parasite species richness of an individual. Even though there are many studies examining the factors that affect parasite species richness, how these factors interact with each other and which ones dominate as predictors of parasite species richness are poorly understood (Lindenfors et al., 2007).

For instance, there are few studies examining the relationship between host genetic factors and host parasite richness. In African freshwater fish, there is some evidence that polyploid species have higher parasite species richness than diploid species (Poulin, 2004). There is also some evidence that there is a negative correlation between parasite species richness and host genetic heterogeneity in freshwater fish (Poulin, 2004). Most studies highlight behavioral and ecological factors rather than genetic factors, and so this review will focus on those rather than the genetic factors. Dense populations of hosts may approximate larger islands, even though their range may not exceed that of less densely populated or social hosts, due to the increased opportunities for transmission.

Social contact can be an important contributor to parasite species diversity because many parasites are spread through direct contact with infected individuals. Therefore, hosts that are highly social or hosts that experience high densities are likely to be infected with more species of parasites (Morand and Poulin, 1998; Lindenfors et al., 2007).

Foraging habits and diet can also have an influence on the number of parasite species that colonize a single host (Vitone et al., 2004). Where hosts forage can greatly influence the number of parasite species that they are exposed to. The actual diet of the host can also affect parasite

exposure. For example, animals that eat invertebrates may have higher parasite species richness than animals with other diets because these invertebrates can serve as intermediate hosts (Vitone et al., 2004). Additionally, percent of leaves in the diet correlates with total helminth parasite species richness, possibly because animals that eat plants are exposed to many directly transmitted parasites as well as accidentally ingested intermediate hosts (Vitone et al., 2004).

Basal metabolic rate may also influence parasite species richness within a host. An increased metabolic rate would lead to increased food intake and as a result, an increased risk of exposure to parasites (Morand and Poulin, 1998). However, basal metabolic rate has proven to be difficult to measure in studies on parasite species richness so relevant data are not available (Morand and Poulin, 1998).

Another factor that influences parasite species richness is host range. A study on the helminth parasites of host waterfowl demonstrated that host range is significantly positively correlated with the number of parasite species richness per host ($p=0.006$) (Gregory, 1990). There is evidence that hosts with larger ranges have increased parasite species richness because they come in contact with more parasites (Lindenfors et al., 2007; Kamiya et al., 2013). A large host range may expose hosts to environmental heterogeneity that supports a greater diversity of parasite species. Also, a larger range likely overlaps with many other host species in comparison to a small range, and each of these additional host species each has their own parasite fauna, some of which may be able to use diverse hosts (Poulin, 2004). This increased exposure to other species of hosts leads to an increased exposure to their parasites (Lindenfors et al., 2007).

Low latitudes are predicted to correlate with higher parasite diversity because there are more resources and higher species diversity close to the equator (Lindenfors et al., 2007; Kamiya et al., 2013). However, this factor can be negatively correlated with other factors such as host

range. One study found that hosts further away from the equator have increased parasite species richness, possibly because host range tends to increase as distance from the equator increases (Lindenfors et al., 2007).

So far, I have reviewed hypotheses associated with space, but time can also affect exposure. Host age can affect parasite species richness because the longer a host has been alive, the more times they have likely been exposed to parasites (Vitone et al., 2004). A study on the intestinal helminthes of bobwhite quail found that age can be an important influence on parasite species richness and density (Moore et al., 1987). Not all studies have shown an increase in parasite species richness as age increases. A negative correlation between host age and parasite species richness has several explanations. First, parasites can be detrimental to a host and therefore highly infected hosts may have shorter life spans (Ezenwa et al., 2006). Also, older hosts may have more developed immune systems that are better able to fight off parasites (Ezenwa, 2006). Additionally, host diet can switch with age. For example, turkey poults eat more insects and arthropods than adults due to higher protein demands (Williams, 1981; Hurst, 1992).

Finally, host size can influence parasite species richness. Host size is the predictor that is most commonly associated with parasite species richness and has been widely studied (Lo et al., 1998; Vitone et al., 2004; Lindenfors et al., 2007; Kamiya et al., 2013). At the individual level, larger and typically older hosts generally have greater parasite density as well as parasite species richness (Kuris et al., 1980). This is analogous to the Island Size Hypothesis. Larger hosts are thought to have both more available space for parasite species to colonize as well as more niches due to their increased size (Lindenfors et al., 2007). Also, larger hosts tend to eat larger quantities of food, which could lead to an increased chance of ingesting parasites (Lindenfors et al., 2007). Larger hosts tend to have longer life spans than smaller hosts, which would allow for

an extended time for parasites to be able to colonize them (Vitone et al., 2004; Kamiya et al., 2013). The relationship between host size and parasite species richness has been extensively studied in fish. In one study, host size was measured as the total length of each coral-reef fish and it was found that the number of ectoparasites was highly correlated with increasing length (Lo et al., 1998). Now that I have explored many different factors that can influence parasite species richness within a host, including social contact, diet, metabolic rate, host range and latitude, and host age and size, I will examine which of these factors have the most support in the literature.

Predictors of Parasite Species Richness

Even though the exact factors that affect parasite species richness are still being studied, four of these factors are commonly invoked to explain the differences in parasite species richness in a host species (Lindenfors et al., 2007). These four factors are host size, host range, host density, and host latitude (Kamiya et al., 2013). A meta-analysis of 62 studies covering animal, plant, and fungal hosts examined these four factors to determine their relative importance in predicting parasite species richness (Kamiya et al., 2013). Kamiya and colleagues found that host species size, host range, and host density are significantly correlated with parasite species richness, and host latitude produced a positive trend, but was not significant (Kamiya et al., 2013). This is an oversimplified view and because these factors are correlated, determining which one or few are actually driving parasite species richness is complicated (Kamiya et al., 2013). Another meta-analysis on parasite species richness in carnivores, thus limiting dietary exposure and phylogeny, also found that host mass, host range, and host density showed the strongest correlation with parasite species richness (Lindenfors et al., 2007). However, this meta-analysis found that parasite richness tended to increase in hosts that lived further from the

equator. This could be because species' host ranges tend to increase further from the equator (Lindenfors et al., 2007). A third meta-analysis examined seven factors that have been predicted to correlate with parasite species richness in hoofed mammals (Ezenwa et al., 2006). This study found that host body size most strongly correlated with parasite species richness, but host population density, host longevity, and social group size were also statistically significant (Ezenwa et al., 2006). Table 1 (below) summarizes these meta-analyses as well as several others. These studies highlight the factors that are emerging as predictors of parasite species richness, but also show that much remains to be evaluated to completely understand these relationships. I will next explore the Island Size Hypothesis as it relates to hosts and their parasites.

Table 1: Meta-analyses examining factors that influence parasite species richness.

| Hosts | Factors Examined | Significant Factors | Authors |
|----------------------------------|---|--|------------------------------|
| Animal Plant Fungal | Host body size Host geographical range Host population density Latitude | Host body size Host geographical range Host population density | Kamiya et al. 2013 |
| Hoofed Mammals | Host body size Longevity of host Gestation length Litter size Host population density Social group size Home range size | Host body size Host population density Longevity* Social group size* | Ezenwa et al. 2006 |
| Carnivores | Host body size Host geographical range Day range Average latitude Diet Population density Mating system | Host body size Host geographical range Distance from equator Population density | Lindenfors et al. 2007 |
| Primates | Host body size Social group size Diet Ranging Behavior | Host body size Social group size | Vitone et al. 2004 |
| Mammal Bird Fish Insect | Group size | Group size | Patterson and Ruckstuhl 2012 |
| Mammals | Host body size Host density | Host body size | Morand and Poulin 1998 |

*= negatively correlated with parasite species richness

Note: Significance value is $p < 0.05$

Island Size Hypothesis

Examining parasite richness across host species provides an opportunity to test the Island Size Hypothesis. Tests of the Island Size Hypothesis have been conducted across many groups of animal and plant hosts. In general, host size correlates with parasite species richness. For instance, multiple studies of monogenean parasites show a strong correlation between freshwater

host fish size and parasite richness. It was found that for 19 species of freshwater fish hosts, 77% of the variation in the number of monogenean species was accounted for by the size of the host (Guegan et al., 1992). Among species of bats, increased mass is correlated with the number of parasitic fly species (Patterson et al., 2008). Host body size in hoofed mammals is also significantly correlated with parasite species richness (Ezenwa et al., 2006).

Some researchers are critical of the methods used in studies that examine host size and parasite species richness. In particular, many of the early studies examining the relationships between host size and parasite richness did not account for phylogenetic effects, which may be due to relatedness and history of host-parasite interactions (Gregory et al., 1996). For example, one study found that there was a positive correlation between host body size and parasite species richness in mammals but did not control for phylogenetic effects (Gregory et al., 1996). However, a different study found that there was no correlation between host body size and parasite species richness when they controlled for phylogenetic effects in mammals (Morand and Poulin, 1998). Yet another study showed that when carnivores alone were considered, overall parasite species richness was correlated with carnivore body size when controlling for phylogenetic effects (Lindenfors et al., 2007).

In summary, there are many factors that can affect the parasite species richness. While host body size may not always be the factor that is most associated with parasite species richness, the quantity of studies showing a correlation between host size and parasite species richness suggests that host size may be one of the few factors that can predict parasite species richness (Morand and Poulin, 1998). This association certainly calls for further experiments.

Caveats in Applying the Theory of Island Biogeography to Hosts

There are multiple cautionary notes to consider when applying the Theory of Island Biogeography to hosts. First, many host traits, such as group size and density, are subject to bias in measurement (Ezenwa et al., 2006). Another problem is that as hosts become larger and older, they are likely to become more infected with parasites. This increased infection may result in disease or death of the host whereas actual islands are not negatively affected by greater species richness (Kuris et al., 1980). In the extreme, if a host dies from these parasites, the island no longer exists. An actual island does not encounter this problem. A third problem in applying the Theory of Island Biogeography to hosts is that hosts have immune and physical responses to defend against parasites while actual islands do not.

A fourth problem is controlling for phylogenetic effects; see above (Morand and Poulin, 1998). Determining the effect of phylogeny on species richness is important to mitigate the effects of inherited parasite species due to common ancestry and instead to focus on parasites acquired as a result of behavioral and ecological factors (Poulin, 2004; Vitone et al., 2004). Controlling for host phylogeny can either cause the relationship between host size and parasite species richness to become less significant or cause it to disappear altogether (Kamiya et al., 2013). Host body size is correlated with many other factors related to ancestry, and this high degree of correlation between these traits could lead to a decrease in the statistical significance of the model (Vitone et al., 2004). However, several methods have been developed to take phylogenetic influences into account so that the ecological factors described earlier can be accurately studied (Poulin, 2004).

In addition to the measurement bias mentioned earlier, another problem to consider when examining the Theory of Island Biogeography is that there is a sampling bias that should be taken into account. Species richness is likely correlated with sampling effort (Morand and

Poulin, 1998; Lindenfors et al., 2007). Hosts that have been studied more likely have more parasites reported (Vitone et al., 2004). In fact, many studies have found that there is a significant correlation between sampling effort and the number of recorded parasite species, which is also true of sampling for all species and not just parasites (Lindenfors et al., 2007). Many studies account for this by including sampling effort in their model by examining citation counts for either host or parasite (Vitone et al., 2004). Sampling bias is a problem to consider with islands in general, not only when applying the theory to parasites and hosts.

Additionally, the distance from an island to the mainland is fixed, while hosts are able to move, thus there is a constantly changing distance between hosts. Hosts also have a long co-evolutionary history with their parasites, while true islands do not have a co-evolutionary history with the species that colonize them.

Despite these challenges, parasites offer an ideal way to study communities and biodiversity. Parasite communities can be easily replicated by studying multiple hosts, the community boundary is clear in the case of infracommunities, and the location within the individual can yield information about relative resource use (Moore and Simberloff, 1990). In addition to this, phylogeny of some parasites may be easier to determine than that of their free living counterparts because some parasites evolve along with their hosts (Kamiya et al., 2013). Also, unlike actual islands, the history and relationships between the host islands can be examined and these data can help to better understand the ecological processes in play (Poulin, 2004).

In conclusion, Island Biogeography Theory and the Island Size Hypothesis can be applied to hosts in order to examine which factors affect parasite species richness. There is evidence that larger hosts have higher parasite species richness due to their increased area.

However, there are multiple problems that may be encountered such as controlling for phylogenetic effects and sampling biases. Now that I have examined Island Biogeography Theory and the Island Size Hypothesis, I will now switch my focus to introduced host species, reintroduced host species, and their parasite communities.

Introduced and Reintroduced Species

Many different species have been introduced to new ranges by humans, which occurs when a species is brought into a geographic area that it previously did not inhabit. These introductions may be deliberate or accidental, and their ecological effects have been widely studied. Species can also be deliberately reintroduced into a historical range when the population has since gone locally extinct, or introduced into contiguous areas that extend their historical boundaries. One of the main reasons that animals are reintroduced into a historical range is for hunting. These reintroductions increase the biodiversity and may help improve the ecosystem while promoting societal interest in the reintroduced species.

Parasites and Introduced or Reintroduced Species

When a new species is introduced to an area, there may be effects on the existing species. With the introduction of animals into an area, there is a risk of transmission of disease between the introduced species and the local species (Oates et al., 2005; Hopkins et al., 1990). The impacts that exotic parasites have on the native species and their parasite communities are influenced by factors such as the rate of encounter, transmission, mortality, and recovery (Telfer and Bown, 2012).

Additionally, there may be effects on the introduced species as well. Parasite release occurs when a host escapes some or all of the parasites from its native habitat when it is introduced to a new area (Torchin et al., 2003; Kelly et al., 2009). In a study involving 26 host

species, on average, an introduced species had half the number of parasite species that the same native hosts did, and the native hosts were also more heavily parasitized (Torchin et al., 2003). For instance, introduced round gobies in the St. Lawrence River had only 8 taxa of helminths while the native logperch was host to 25 taxa and the native spottail shiner was host to 24 taxa (Gendron et al. 2012). Similarly, parasite species richness, parasite prevalence, and parasite intensity were all significantly higher in native Puerto Rican coqui frogs than in the same species in Hawaii where the species is invasive (an introduced species that affects the ecosystem in a negative manner) (Marr et al., 2008). A study done by Ross et al. on European slugs showed that nematodes were present at 93% of the study sites in the UK while they were present at only 34% of sites in the US where the slugs are invasive (Ross et al., 2010). Studies such as these have led to the hypothesis that introduced species tend to thrive in their new habitats because they have a lower parasite burden than the native hosts (Torchin et al., 2003). Parasite release is enabled by the limitation of parasites establishing in a new area. Many parasites do not live through either the bottleneck of having so few hosts and/or parasites introduced or the new environmental conditions. Additionally, many have complex life cycles that involve multiple hosts in order to complete all life stages. In the new environment, it is unlikely that all the hosts will be present, and therefore the parasite cannot establish (Torchin et al., 2003). The introduced host population may also be very small and all the introduced hosts may not be infected. These small introduced populations may also lead to bottlenecks (Torchin et al., 2003).

While introduced species tend to have fewer parasite species than native species, they often retain at least some of their parasites. Parasite spillover occurs when an introduced host introduces parasites to a new native host species (Kelly et al., 2009). However, not all parasites will be able to spill over into the native populations; they can be limited by factors like host

specificity of the parasites and host community composition, in addition to the factors listed above (Holt et al., 2003; Hatcher et al., 2012).

Parasite spillback occurs when a species is introduced into a new area and the introduced species acts as a competent host for native parasites (Kelly et al., 2009; Telfer and Bown, 2012). In this case, the introduced host can become a reservoir for the native parasites that they acquire and spill the parasites back to the native hosts (Kelly et al., 2009; Telfer and Bown, 2012). If the introduced species is a competent host for the native parasites, then there may be an amplification effect, that is, the parasite may become more prevalent. However, if the introduced species is not a competent host for the native parasite, spillback will not occur and the introduced host may even reduce parasite levels in the native hosts causing a dilution effect (Kelly et al., 2009; Telfer and Brown, 2012). Even though the hosts are generally colonized by the native species of parasites, introduced hosts still have fewer parasites than native hosts (Torchin et al., 2003).

The introduction and transmission of parasites is especially important to consider with regard to wild turkeys because there are many diseases that can be transmitted to domestic chickens and turkeys, or other wild birds. These parasites include *Histomonas meleagridis*, *Salmonella enteria*, *Mycoplasma sp.*, and helminths (Oates et al., 2005). For instance, turkeys that appear healthy can be carrying *Mycoplasma gallisepticum* and can transmit this organism to uninfected turkey populations or to domestic poultry populations. This bacterium causes sinusitis and a decrease in egg production (Fritz et al., 1992). I will discuss the parasites of wild turkeys further later in this text.

Wild turkeys are not invasive to Colorado since they were historically present, declined, and then population numbers increased. Due to this history of reintroduction, we can use them as

a model of an invasive or introduced species to try and determine whether any of these processes (parasite release, parasite spillover, and parasite spillback) are at work in terms of the parasite communities and how they have developed. Now, I will summarize wild turkey history and biology before reviewing the common parasites of these birds.

Wild Turkey History and Background

History:

Fossils of turkey bones have been found dating back to the Upper Pliocene, the most ancient of which were found in Southwestern Kansas (Aldrich, 1967). Wild turkeys were an important food source for some Native Americans, while others kept turkeys for their feathers (Aldrich, 1967). There is evidence of domestication of wild turkeys by the Pueblo in Southwestern Colorado, Southern Utah, and Northern Arizona (Aldrich, 1967). By the time Europeans settled in America, turkeys were abundant (Williams, 1981). In the 1520s, the domestic turkey arrived in Spain and by 1530 it was well established in Europe (Aldrich, 1967; Kennamer et al., 1967). Over next 400 years the domestic turkey became established (Aldrich, 1967). In the 1920s commercial domestic turkey operations started to replace small farm-raised turkey operations and by 1941, domestic turkeys were a primary agricultural industry in the United States (Kennamer et al., 1967). Domesticated turkeys are now present worldwide.

Wild turkeys are endemic to the southern and eastern United States as well as north-central Mexico (Thornton et al., 2012). Even though the exact timing of wild turkey domestication is still unknown, recent research has demonstrated that domestication happened in both Mesoamerica and the American Southwest (Thornton et al., 2012). Perhaps due to domestication or to captive rearing, wild turkeys successfully spread across the United States. Wild turkeys experienced a widespread decline in numbers in the early 1900s due to human

activity such as overhunting and habitat loss (Mitchell et al., 2011). However, it is possible that blackhead disease, which spread from domestic operations to wild turkeys, could have contributed to the decline of the wild turkey (Aldrich, 1967).

A review of the known history of wild turkeys in the United States may illuminate why studying the parasite communities of wild turkeys is so intriguing. The wild turkey was originally found in 39 states; by the 1920s only 18 of those states still had wild turkeys, and many of the states in which they remained had only very small numbers (Kennamer et al., 1967). Reports show that the last wild turkey in Illinois was shot in 1905 (Smith, 2009). In 1937, The Wildlife Society was formed, and the Pittman-Robertson Wildlife Restoration Act was enacted (Williams, 1981). By the 1940s, only tens of thousands of turkeys remained in the US (Dickson, 1992). During this time, it is estimated that the wild turkey only occupied about 12% of its former range; in the east there were small populations in the west as well (Williams, 1981). In 1941, a live trap and release program was started in Colorado (Aldrich, 1967). One study shows that from 1941 to 1962, 1293 wild turkeys in Colorado were trapped and released to other areas. Only 134 of these wild turkeys were sent to other states; instead, many of them were relocated to north-central Colorado (MacDonald and Jantzen, 1967). By 1948 the wild turkey was no longer present in 15 states where it was originally found (Williams, 1981). In 1950 wild turkeys from Colorado were relocated to South Dakota, and from 1952 to 1959, Colorado turkeys were relocated to Utah (MacDonald and Jantzen, 1967). By 1958, wild turkeys had been restocked to most of the original states and even beyond their historic range (Williams, 1981). In 1958 there were an estimated 8,000 wild turkeys in Colorado (MacDonald and Jantzen, 1967). By the 1960s, some states (<20) were starting to have hunting seasons again (Kennamer et al., 1967). In 1961, some Colorado wild turkeys were moved to Oregon and also during 1961, they were

transported to Idaho (MacDonald and Jantzen, 1967). In 1991, there were wild turkey hunting seasons in all 48 contiguous states as well as in Hawaii (Keck and Langston, 1992). In 1992, there were an estimated four million wild turkeys in the United States (Dickson, 1992).

Wild turkey population estimates are often made by road-based distance sampling. One study demonstrated that this technique yielded fairly accurate results as long as the sampling was conducted during the morning or afternoon from December to March. This study concludes that more studies need to be done on turkey populations around roads in order to obtain the most accurate surveys (Erxleben et al., 2011).

Wildlife management programs have been working for the past fifty years to help wild turkeys expand back into their historical ranges through massive reintroduction efforts (Oates et al., 2005; Mock et al., 2001). These reintroductions have been very successful, and now the wild turkey's range extends beyond its original range. Since wild turkeys are important game birds, these reintroductions have been important in order to keep turkey hunting seasons open. The number of hunters in the United States is decreasing, but interestingly, the number of turkey hunters is rising, as is the number of turkeys that are harvested during the hunting seasons (Chamberlain et al., 2012). One study in Louisiana showed that there was a 2-fold increase in male turkey survival when bag limits and the hunting season were decreased (Chamberlain et al., 2012). In the future, more studies should examine how different harvest regimes affect wild turkey survival and turkey population maintenance.

Unfortunately, the reintroduction efforts in Colorado have been poorly documented, and often turkeys were transplanted by turkey enthusiasts without much documentation. Nonetheless, turkeys now cover a large portion of Colorado and have a stable population that allows hunting.

Taxonomy:

Wild turkeys (*Meleagris gallopavo*) belong to the order Galliformes, the family Phasianidae, and the subfamily Meleagridinae. In 1758, Linnaeus gave the wild turkeys the scientific name *Meleagris gallopavo*. “*Meleagris*” is Greco-Roman for guinea fowl, and “*gallopavo*” is Latin for peafowl (Kennamer et al., 1967).

Subspecies:

There are two species of turkey: *Meleagris gallopavo* is the wild turkey, and *Meleagris ocellata* is the Ocellated turkey, found in the Yucatan Peninsula. There are many subspecies of wild turkeys, five of which are native to North America. These include the Rio Grande (*Meleagris gallopavo intermedia*), Merriam’s (*Meleagris gallopavo merriami*), Osceola or Florida wild turkey (*Meleagris gallopavo osceola*), Gould’s (*Meleagris gallopavo mexicana*), and the Eastern wild turkey (*Meleagris gallopavo sylvestris*), as well as several variations of hybridized turkeys (Stangel et al., 1992; Mitchell et al., 2011). The subspecies vary in physical appearance, but the subspecies designation is based mostly on geography (Williams, 1981). These subspecies often interbreed and their identification can be very subjective (Stangel et al., 1992). Natural selection and the founder effect are possible explanations for the variation in wild turkeys (Stangel et al., 1992).

The average weight of wild turkeys can vary by subspecies. Data collected from adult males shows that the average weights are: 17.8-18.3 pounds for Merriam’s, 16.93-20 pounds for Eastern, 17.5 pounds for Rio Grande, and 14.5 pounds for Florida wild turkeys (Lewis, 1967). Colorado has two of these sub species of turkeys, the Merriam’s wild turkey (*Meleagris gallopavo merriami*) and the Rio Grande wild turkey (*Meleagris gallopavo intermedia*) (MacDonald and Jantzen, 1967).

Merriam's Wild Turkey

The historic range of Merriam's wild turkey included Colorado, New Mexico, Texas and Arizona, where they are still present (Shaw and Mollohan, 1992; Mock et al., 2001). There are various hypotheses about the evolution of this subspecies of wild turkey. For instance, Merriam's wild turkeys could be descendants of birds brought to the area by Pueblo cultures, they could be derived from Eastern or Gould's subspecies, or they could be related to the Rio Grande wild turkeys (Shaw and Mollohan, 1992). Very few parasite studies have been done on Merriam's wild turkey (MacDonald and Jantzen, 1967).

Rio Grande Wild Turkey

The Rio Grande wild turkey differs in appearance from the other subspecies because the tips of the tail feathers are tan (Beason and Wilson, 1992). The Rio Grande wild turkey historically inhabited Mexico, Oklahoma, and Kansas. Currently, the range of the Rio Grande wild turkey stretches from California to North Dakota (Schmutz and Braun, 1989). Relocation efforts have been successful in creating a stable population of Rio Grande wild turkeys in Colorado. Between 1980 and 1983, sixty Rio Grande wild turkeys were transplanted to Logan, Morgan, and Washington counties along the South Platte River (Schmutz and Braun, 1989). These turkeys were obtained from Kansas and Texas (Schmutz and Braun, 1989).

Diet:

Information about the diet of turkeys is obtained from food data gathered by observation of turkeys, dissections of the crop and gizzard, and analysis of droppings (Korschgen, 1967). Therefore, these data may not be complete. In the case of observation, some observations may be erroneous or missed altogether. In the case of gastrointestinal contents, variability in the rate of

digestion means that some foods digest to a point of being unrecognizable while others are overrepresented.

Turkeys use the gizzard to grind up food and this often also includes use of grit, or small rocks and sand that are swallowed in order to help grind up and digest the food (Williams, 1981; Korschgen, 1967). Overall, the diet of wild turkeys depends on the age of the turkey and the season (Hurst, 1992). The diet can also vary by subspecies, which may be in part due to geographic differences of these subspecies (Hurst, 1992). Turkeys are opportunistic omnivores, and there is a great amount of variation in the food that is consumed (Hurst, 1992). The following account illustrates this variation in diet:

“In Mississippi, I have seen a gobbler’s crop full of acorns, one full of galls from wild azalea, one full of rye grass, one full of sedge (*Carex* sp.) leaves and seeds, one full of newly germinated pine seeds, one full of unripe fruit of rusty blackhaw (*Viburnum rufidulum*), and 2 jakes that had eaten many insects (adults, larvae, and pupae) and green anoles (lizards) (Hurst 1989). One hunter harvested a gobbler in a flooded bottomland hardwood forest and was surprised to find that the gobbler had been feeding on crayfish! A brood hen killed by a great horned owl had eaten 23 periodical cicadas. Another hen ate 21 snails, while other hens had gorged on blackberries” (Hurst, 1992).

Wild turkeys are opportunistic omnivores and have a varied diet depending on what is available (Williams, 1981). Wild turkey poults and adults have similar eating habits; poults primarily eat insects and arthropods due to higher protein demands, supplemented with plant material (Williams, 1981; Hurst, 1992). The diet of adult turkeys is also largely composed of plant material, including grasses, seeds, grains, nuts, and fruits (Hurst, 1992). These plant materials account for 90% of the adult diet (Korschgen, 1967; Williams, 1981). However, many other food items are also found in the crop including animal foods such as insects, spiders, ticks, millipedes, centipedes, snails, slugs, crustaceans, etc. (Korschgen, 1967; Hurst, 1992). Food

availability is also seasonal. In the summer, wild turkeys eat more insects, while in the fall they consume more nuts and fruits (Williams, 1981).

In Colorado, bluegrass is an important component of the diet, but animals also figure prominently into the diet. For instance, one study showed that in the fall, 20% of the diet of turkeys in Colorado is animal foods (Korschgen, 1967). Out of 1,545 turkeys found in Colorado, 76.5% contained grass leaves, 35.6% contained forb leaves, 19.4% contained pines, 20.2% contained dandelion, and 40.2% contained animal foods which were mostly insects. Smaller amounts of many different food items were also found, such as acorns, roses, needle grasses, cactus, corn, sunflowers, etc. (Korschgen, 1967).

Reproduction:

Wild turkeys are promiscuous breeders; only the hens take care of the nests and have parental duties, while toms do not contribute to parenting (Healy, 1992; Williams, 1981). Males mostly gobble in the spring during mating season (Williams, 1981). Once a female is within eyesight of the male, he will proceed to strut, and then mating will occur if the female is receptive (Williams, 1981). Only one male in each coalition will mate and one study demonstrated that these coalitions are composed of related individuals, and that there is kin-selected indirect fitness for the subordinate turkeys in the coalitions (Krakauer 2005).

Nests are shallow depressions on the ground generally with concealing vegetation (Williams, 1981; Healy, 1992; Locke et al., 2012). The nests are built over several days while the eggs are being laid. Each time a hen lays an egg, she covers it with nesting material, and this material builds up to form the nest (Williams, 1981). The clutch size is between 6-17 eggs, with the average clutch having 11 eggs (Williams, 1981; Healy, 1992). The clutch size can also vary depending on subspecies. Different sources cite different clutch sizes, generally in the vicinity of

10-12 eggs per clutch (Bailey and Rinell, 1967). Eggs will hatch around 28 days after the hen starts incubating them (Bailey and Rinell, 1967; Williams, 1981). Poults use a process called pipping to hatch, in which they use a specialized egg tooth to make the first hole and open the shell (Williams, 1981). Poults will imprint on their mother once they have hatched (Healy, 1992). Wild turkey hens raise only one brood per year. However, they are likely to nest again if their nests are destroyed (Williams, 1981).

Behavior:

Wild turkeys live in flocks, which consist of a few hens and their young (Bailey and Rinell, 1967). There are also flocks of males (Bailey and Rinell, 1967). Toms exhibit a dominance hierarchy in flocks, and turkeys fight in order to establish their position within the flock (Bailey and Rinell, 1967; Williams, 1981; Healy, 1992). Once poults hatch, they grow quickly and are soon able to do most adult activities like eating, flying, roosting, scratching, and dusting (Healy, 1992). A typical day for a turkey consists of waking up with the sun, spending the morning feeding, resting for a while, dusting, feeding again in the afternoon and evening, and then roosting in trees at night (Williams, 1981). Wild turkeys are non-migratory birds and normally there is no more than one to two miles between summer and winter ranges (Williams, 1981). The wild turkey speed depends on the type of locomotion. They walk at around 3 miles per hour, run at about 19 miles per hour, and can fly at 55 miles per hour, but they can only fly up to half mile (Williams, 1981). The lifespan is about 12 years in captivity, and generally shorter than that in the wild (Bailey and Rinell, 1967). The two main habitat requirements for wild turkeys are trees, to provide cover and roost, and grass for food (Healy, 1992).

Parasites of Wild Turkeys

Few diseases are clinically prevalent in wild turkeys, and those that are of concern for wild turkeys are generally diseases from pen raised or domestic poultry (Markley, 1967; Blankenship, 1992). Wild, domestic, and pen raised turkeys show an increased number of parasites when turkeys are more crowded (Markley, 1967). Some of the concerns surrounding pen raised and domestic turkeys are decreased genetic diversity, disease introduction to native wild turkeys, disease introduction from turkeys released into the wild, or diseases introduced to domestic turkeys by wild turkeys (Davidson and Wentworth, 1992). Climate is a major influence on parasite load of domestic poultry. The heterogeneity of the major histocompatibility complex (MHC) is higher for wild turkeys than for domestic turkeys, therefore domestic turkeys could have a lower ability to generate an immune response (Husby et al. 2011).

Wild turkeys are host to many different parasites; most of these cause subclinical infections and very few cause disease or mortality (Davidson and Wentworth, 1992). Some effects of parasites are the loss of nutrients, damage to the intestines and other organs, loss of blood, secondary infections, and behavioral changes such as a higher likelihood to leave the nest (Oates et al., 2005). Wild turkeys can also become infected with external parasites such as ticks, mites, lice, and flies (Markley, 1967; Davidson and Wentworth, 1992).

Viruses, Bacteria, and Fungi

Wild turkeys can be infected with viral, bacterial, fungal, and parasitic diseases (Davidson and Wentworth, 1992). One common viral infection in wild turkeys is avian pox (*Avipoxvirus*) (Davidson and Wentworth, 1992). There are multiple bacterial infections experienced by turkeys, including infection with *Mycoplasma sp.* causing a disease of domestic poultry (Davidson and Wentworth, 1992). *Mycoplasma gallisepticum* infects turkeys, chickens,

and other galliforms causing respiratory symptoms and swollen sinuses with caseous exudate and can also cause a decrease in the percentage of eggs that hatch in wild turkeys (Davidson and Wentworth, 1992). *Mycoplasma iowae* may also be found in wild turkeys and other domestic poultry and depending on the pathogenicity of the strain, may cause decreased hatch rates and leg abnormalities in turkey poults (Wood and Wilson, 2013). *Salmonella enterica* is another bacterial infection found in both wild and domestic birds, including turkeys (Davidson and Wentworth, 1992). Botulism (*Clostridium botulinum*) can also cause disease in turkeys and there have been documented losses of turkeys in Utah due to a contaminated waterhole (Markley, 1967). *Aspergillus sp.* causes a fungal infection in wild turkeys that often affects the respiratory tract (Markley, 1967; Davidson and Wentworth, 1992).

Protozoa

Wild turkeys can be infected with various protozoan parasites. One of the most important protozoans for turkeys in terms of disease is *Histomonas meleagridis*, which causes Blackhead disease in many galliform birds including domestic poultry. Infections with *H. meleagridis* cause necrosis and ulceration of the cecal mucosa and liver. Transmission can occur via a cecal nematode vector (*Heterakis gallinarum*). Coccidiosis is another protozoan disease caused by parasites in the genus *Eimeria* (Davidson and Wentworth, 1992).

Helminths

Helminth parasites are commonly detected in wild turkeys, but helminth infections are typically subclinical. Additionally, one study suggests that within wild turkey hosts, there does not appear to be a pressure to develop genetic resistance to helminths due to the lack of correlation between epigamic characters and helminth abundance (McJunkin and Zelmer, 2008).

Many studies have been conducted on the intestinal parasites of wild turkeys, but the vast majority of these studies focus on the eastern subspecies (*Meleagris gallopavo silvestris*); the parasite populations of western states are not as well documented (McJunkin et al., 2003). Not only have few studies been conducted on western subspecies of wild turkeys, but there are no studies of any galliform in Colorado, except for one study on hematozoa in sage grouse and another of coccidian in both white-tailed ptarmigan and blue grouse (Stabler et al., 1977; Stabler et al., 1979). To my knowledge, there have been no studies done on the parasites of the wild turkeys in Colorado. There have also been very few regional comparisons of wild turkey parasites. One study by Castle and Christensen (1984) compared the helminth populations from 11 southeastern states. As far as I know, no studies have compared the differences between the parasite communities in the central part of the US and the east coast.

Based on studies from nearby areas, I have established a list of possible parasites that could be found in wild turkeys. Studies done in Kansas, Nebraska, Kentucky and Tennessee have found parasites from class Cestoda, phylum Nematoda, class Trematoda, and phylum Acanthocephala within the intestinal tracts of wild turkeys (Oates et al., 2005; McJunkin et al., 2003; Castle and Christensen, 1984). In my study, I focused on helminth parasites, so I will explore these helminths in greater depth below.

Cestodes

Cestoidea is the class that contains the tapeworms, which are flat and segmented. Adult cestodes typically live in the intestines of vertebrates and have also been found in invertebrates. Cestodes have no mouth or alimentary canal and they absorb their nutrients from their host's intestinal contents across their tegument (Markley, 1967). They have a scolex that attaches the cestode to the intestinal mucosa, a neck, and strobila which contains individual reproductive

segments called proglottids. Each proglottid is formed by a process known as strobilation. Thereafter, the proglottids become sexually mature, copulation occurs, eggs are produced and gravid proglottids and/or eggs detach to be shed in the feces (Roberts and Janovy, 2009).

Many different species of cestodes have been documented in wild turkeys, but none are associated with more than mild pathology (Davidson and Wentworth, 1992). All cestodes that infect turkeys need intermediate hosts, which is typically an invertebrate (Davidson and Wentworth, 1992).

Nematodes

Nematoda is one of the most speciose phyla. These are typically bilaterally symmetrical with tapered ends and are covered in a cuticle. They are usually dioecious and sexually dimorphic (Roberts and Janovy, 2009).

Most nematodes that infect wild turkeys are not pathogenic, but there are a few that are very pathogenic (Davidson and Wentworth, 1992). One nematode is of particular interest for poultry disease studies, *Heterakis gallinarium*. This cecal worm has been found in turkeys and although it is not necessary for transmission of *Histomonas meleagridis*, it is that protist's main vector and reservoir. *H. meleagridis* causes blackhead disease, which can be lethal in a relatively short time period, ranging from 10-31 days post exposure to the parasite (Hu and McDougald, 2003). It appears that *H. gallinarium* is necessary for *H. meleagridis* to survive outside the host and for transmission between flocks. In the absence of *H. gallinarium*, *H. meleagridis* can continue to cause disease in a flock (Hu and McDougald, 2003).

Trematodes

Trematodes, also known as flukes, are dorsoventrally flattened and they have an oral sucker; some also have an acetabulum. In a typical trematode life cycle, an adult fluke lays an egg, which hatches to become a miracidium that enters the first intermediate host, typically a snail (Markley, 1967; Davidson and Wentworth, 1992). In the snail, the miracidium becomes a sporocyst which then develops multiple redia. Each redia liberates countless cercariae, which exit the host. The cercaria will then encyst in a second intermediate host or on vegetation, becoming a metacercaria, which is infective to the definitive host (Roberts and Janovy, 2009). There are numerous variations of this life cycle. Trematodes that infect wild turkeys have not been found to be pathogenic (Davidson and Wentworth, 1992). Those found in wild turkeys all have adhesive organs and typically involve a snail/mollusk first intermediate host (Markley, 1967).

Acanthocephalans

Parasites in the phylum acanthocephala are often called thorny-headed worms due to the spiny proboscis that attaches to the intestine of the host (Roberts and Janovy, 2009). Acanthocephalans are nonsegmented. Acanthocephalans from the genus *Mediorhynchus* have been found in turkeys, but these infections are rare and are sometimes considered accidental infections. Acanthocephalans typically produce subclinical infections in turkeys (Davidson and Wentworth, 1992).

Broad ecological concepts such as Island Biogeography Theory and invasion biology clearly inform the study of wild turkey parasite communities. Applying Island Biogeography Theory and the Island Size Hypothesis to hosts and their parasites because examining parasite biodiversity is an important aspect of ecology, due to parasites making up a large percentage of

overall biodiversity. Additionally, invasion biology including parasite release, parasite spillover, and parasite spillback, may play a part in the parasite communities of wild turkeys in the United States due to the wild turkeys' history.

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CHAPTER 2: The Theory of Island Biogeography as Applied to the Helminth Parasites of Galliform Hosts

Summary

The Theory of Island Biogeography can be applied to hosts in order to examine the factors that affect parasite species richness. Hosts can be considered islands on three levels: individual, group, or species. When considering an individual host as an island, there are many different factors that can influence parasite species richness. Host size, host range, host density, and host latitude are the best supported factors that influence parasite species richness. The Island Size Hypothesis suggests that larger sized hosts are expected to have higher parasite species richness due to an increased area for parasites to occupy. When considering host species as islands, galliform birds offer an opportunity to study the Island Size Hypothesis since they exhibit large interspecific variations in size and because they are well studied game birds. In addition, they are non-migratory, so their parasites are acquired locally. Twenty four studies of seventeen galliform species and their helminth parasites were reviewed and analyzed to test the Island Size Hypothesis. These data suggest that there is a positive correlation between host body size and parasite species richness in galliform birds ($R^2 = 0.212$). Also, the best supported model consists of both galliform mean mass and family. This model also shows a positive relationship. More studies should be done in order to further understand the factors that influence parasite species richness.

Galliform Birds and the Theory of Island Biogeography

In order to better examine the Theory of Island Biogeography, and more specifically the Island Size Hypothesis, I performed a meta-analysis of parasite communities found in the order Galliformes. Although galliforms have differing reproductive strategies and ranges, they are

similar in that they are game birds, as the order includes wild turkeys, chickens, quail, and pheasants as well as many other species. Because these birds are often hunted or bred, they are well studied in terms of their ecology, including their parasite species. These birds also tend to stay close to the ground, flying only short distances and they are non-migratory, which also provides a unique opportunity to study their local parasite fauna (Brennan, 1999). Galliform birds offer an appropriate opportunity to examine the Island Size Hypothesis because of the amount of literature on the parasite fauna of many of the species as well as the large differences in the sizes (90-7800g) of galliform birds (Eaton, 1992).

Helminths

Parasitic worms, also known as helminths, comprise cestodes, nematodes, trematodes, and acanthocephalans. Helminths are found in the vast majority of all taxa. The host and parasite characteristics can influence the number of parasite species found within a particular host species (Vitone et al., 2004). Helminths can have large impacts on the abundance and evolution of a host species and therefore it is important to understand parasite communities in order to be able to better understand wildlife communities as whole (Vitone et al., 2004).

Materials and Methods

I reviewed twenty six studies of the helminth parasite communities of nineteen species of galliform birds. These species are Common Quail (*Coturnix coturnix*), Northern Bobwhite (*Colinus virginianus*), California Quail (*Callipepla californica*), Scaled Quail (*Callipepla squamata*), White-tailed Ptarmigan (*Lagopus leucura*), Hazel Grouse (*Bonasa bonasia*), Barbary Partridge (*Alectoris barbara*), Red-legged Partridge (*Alectoris rufa*), Rock Ptarmigan (*Lagopus muta*), Willow Ptarmigan (*Lagopus lagopus*), Swainson's Spurfowl (*Pternistis swainsonii*), Lesser Prairie Chicken (*Tympanuchus pallidicinctus*), Greater Prairie Chicken (*Tympanuchus*

cupido), Black Grouse (*Tetrao tetrix*), Kalij Pheasant (*Lophura leucomelanos*), Helmeted Guineafowl (*Numida meleagris*), Ring-necked Pheasant (*Phasianus colchicus*), Capercaillie (*Tetrao urogallus*), and the Wild Turkey (*Meleagris gallopavo*). I searched for studies using Web of Science and Google Scholar. Key words included the following: galliform, helminth, parasite, intestinal, community, as well as various species names. The references of these papers were also used to find additional sources.

From each of these papers, the number of helminth parasite species was recorded. The CRC Handbook of Avian Masses was used to obtain the average mass of each galliform host. The data were compiled in Table 2.1 and were analyzed to examine the correlation between host mass and parasite species richness (as measured by the total number of helminth species within a given host species). When there were multiple studies of a single host species, the mean number of helminth species was calculated (numspecies). In some cases, data were not available for both male and female mass and therefore the mean mass was calculated (meanmass). The equation of the regression line as well as the R^2 value were calculated in Microsoft Excel for the relationship between mean number of species and mean mass. The data were also analyzed in SAS in order to further explore the relationships between the variables. Family was included as a variable in order to account for phylogeny. Several models were tested under a Poisson distribution. First, the model including just the intercept was tested, in which the null hypothesis is that there is no effect. Other models included meanmass, family, and meanmass+family. These models were used to ask which variables influence the mean number of helminth parasite species.

Table 2.1: Host species, weight, and number of helminth species.

| Host | Mean Mass (g) | Mean # of Helminth Species | References |
|---|----------------------|-----------------------------------|---|
| Common Quail / <i>Coturnix coturnix</i> | 96.5 | 5 | Kurtpinar, 1957 |
| California Quail / <i>Callipepla californica</i> | 174 | 5 | Moore et al., 1983 |
| Northern Bobwhite / <i>Colinus virginianus</i> | 178 | 12 | Moore and Simberloff, 2000 |
| Scaled Quail / <i>Callipepla squamata</i> | 184 | 8 | Landgrebe et al., 2007 |
| White-tailed Ptarmigan / <i>Lagopus leucura</i> | 360 | 5 | Babero, 1953 |
| Barbary Partridge / <i>Alectoris barbara</i> | 418.5 | 7 | Foronda et al., 2005 |
| Hazel Grouse / <i>Bonasa bonasia</i> | 429 | 4 | Isomursu et al., 2006 |
| Red Legged Partridge / <i>Alectoris rufa</i> | 528 | 14 | Millan et al., 2004 Calvete et al., 2003 |
| Rock Ptarmigan / <i>Lagopus muta</i> | 535.5 | 6 | Babero, 1953 Skirnisson et al., 2012 |
| Willow Ptarmigan / <i>Lagopus lagopus alascensis</i> | 569 | 6.5 | Babero, 1953 Holmstad and Skorping, 1998 |
| Swainson's Spurfowl / <i>Francolinus swainsonii</i> | 605.5 | 6 | Owen et al., 2008 |
| Lesser Prairie Chicken / <i>Tympanuchus pallidicinctus</i> | 746 | 3 | Pence and Sell, 1979 |
| Greater Prairie Chicken / <i>Tympanuchus cupido pinnatus</i> | 864 | 5 | Harper et al., 1967 |
| Kalij Pheasant / <i>Lophura leucomelanos</i> | 894.5 | 1 | Lewin and Mahrt., 1983 |
| Black Grouse / <i>Tetrao tetrix</i> | 1067.5 | 4 | Isomursu et al., 2006 |
| Ring-Necked Pheasant / <i>Phasianus colchicus</i> | 1135 | 4 | Dowell et al., 1983 |
| Helmeted Guineafowl / <i>Numida meleagris</i> | 1299 | 16.3 | Vercruyssen et al., 1985 Junker and Boomker, 2007 Owen et al., 2008 |
| Capercaillie / <i>Tetrao urogallus</i> | 2950 | 4 | Isomursu et al., 2006 |
| Wild Turkey / <i>Meleagris gallopavo</i> | 6050 | 18 | McJunkin et al., 2003 Donnelly, 2005 Oates et al., 2005 |

Results

Mean mass showed a positive correlation with mean parasite species richness, see Figure 2.1. The R^2 value calculated as 0.212 and the equation of the regression line calculated as $y=0.0016x + 5.4836$. The model including both meanmass and family had the lowest AIC_c value (109.90). Both family and meanmass contribute significantly to the model, and meanmass was the most significant (p-value=0.0006) (Table 2.2).

Figure 2.1: Mean Host Species Mass and Mean Number of Helminth Species in Galliform Birds

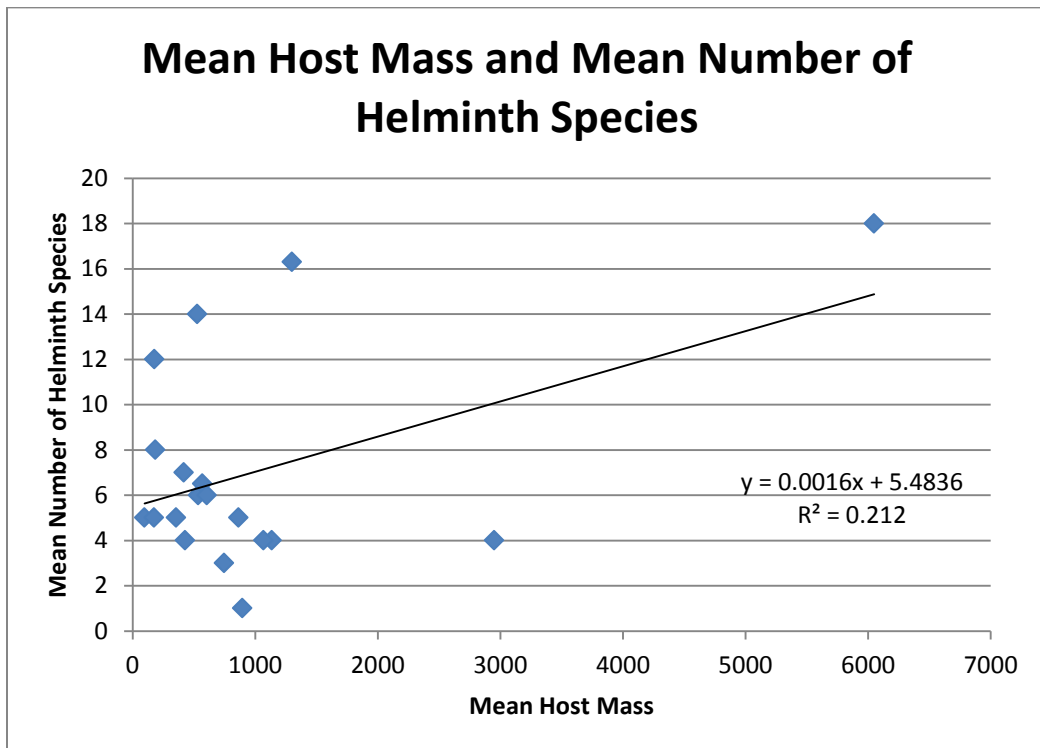


Table 2.2: Results from SAS for Various Models (Intercept only, Meanmass, Family, Meanmass+Family), showing that the lowest AIC_c value is the model containing both meanmass and family

| Model | Max. Log Likelihood | AIC _c |
|-----------------|---------------------|------------------|
| Intercept only | -57.51 | 117.26 |
| Meanmass | -53.55 | 111.85 |
| Family | -54.50 | 116.59 |
| Meanmass+Family | -49.52 | 109.90 |

Discussion

These data support the predictions of Theory of Island Biogeography as reflected in the Island Size Hypothesis applied to galliform birds. The regression shows that there is an overall positive trend between galliform mass and number of helminth species. Also, the best supported model with the lowest AIC_c value included both meanmass and family, which suggests that mass and number of parasite species are related. Galliform mean mass is the most significant contributor to the model (p-value=0.0006). However, the positive correlation between galliform host mass and the number of parasite species is highly driven by one point, the wild turkey (see Figure 2.1). Therefore, this relationship should be further evaluated to see if there really is a trend when the wild turkey is not considered. Further analysis will determine if this correlation is driven by the wild turkey, or if the possible addition of other species, as discovered in the literature, will alter the results. This positive relationship could reflect several factors. First, as stated in the Island Size Hypothesis, larger animals have more volume and surface area and therefore may have more parasites species and higher parasite intensity. These larger animals may also eat more and come in contact with more parasites. Larger animals themselves may also

have larger parasites which would be easier to detect, or the larger animals may be more studied creating a sampling bias.

A more elaborate analysis (e.g., independent contrasts) should be conducted that takes into account both host phylogenetic effects as well as sampling bias. This analysis should include more host species in order to better represent the Order Galliformes. Transmission mode may also affect which factors influence parasite species richness, and this should be explored further. In particular, sexually transmitted parasites tend to be understudied in non-human animals (Freeland, 1979). Whether parasites are endoparasitic or ectoparasitic may also impact which factors influence parasite species richness and these differences should be studied and noted (Kamiya et al., 2013).

Conclusions

Overall, examining the Theory of Island Biogeography as it relates to parasites can be important for determining factors that affect species richness. The Theory of Island Biogeography can also be applied to zoonotic diseases and epidemiology. Factors such as host island size and host island distance can influence how disease is spread and how common certain diseases are. For example, global travel and urbanization have led to a decrease in distance between human populations, which may be factors that facilitate spread of human pathogens such as HIV or SARS (Reperant, 2010). We should continue to study the factors that affect parasite species richness in order to better understand ecosystems so that we can use this information to enhance management strategies and mitigate zoonotic diseases.

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CHAPTER 3: Gastrointestinal Helminths from Wild Turkeys (*Meleagris gallopavo*) in Colorado

Summary

This study examined the gastro-intestinal parasites of wild turkeys in Colorado in order to better understand the parasite community structure within Colorado wild turkeys. The intestines of 24 wild turkeys obtained by hunters in Colorado were examined. Three species of cestodes (*Hymenolepis sp.*, *Imparmargo baileyi*, and *Metroliasthes sp.*), one species of trematode (*Echinoparyphium sp.*), one species of acanthocephalan, as well as two species of nematodes (*Heterakis sp.* and a partial specimen of a second species) were identified. Since the population of wild turkeys in Colorado has fluctuated, this study also presents an opportunity to look at parasite colonization of a reintroduced host species as well as parasite escape and parasite spill back.

Introduction

Wild turkeys once thrived and had a widespread range across the United States. In the early 1900s they experienced a massive decline potentially caused by habitat loss and over hunting (Mitchell et al., 2011). Since then, massive reintroduction efforts have helped turkeys to reestablish their historical range and their present range is now larger than the historic range (Mock et al., 2001; Oates et al., 2005). Due to these efforts, there is a well-established population of wild turkeys in Colorado that supports hunting, as regulated by Colorado Parks and Wildlife. Both Merriam's (*Meleagris gallopavo merriami*) and Rio Grande (*Meleagris gallopavo intermedia*) subspecies of wild turkeys live in Colorado. Unfortunately, Colorado is among many places where reintroduction efforts were poorly documented. Therefore, few records exist that shed light on the origin of Colorado turkeys.

Studying parasite communities of a host that has been reintroduced to a prior habitat can be very enlightening because examining which parasites they have obtained since being reintroduced can give scientists an insight into the relationships between invasive species and their parasite communities. Parasite spillback and parasite escape can greatly affect establishment of invasive species, and they can also affect the likelihood of reintroduction success.

To the best of my knowledge, no previous study has examined the intestinal parasites of wild turkeys in Colorado, but studies have been done in bordering states such as Kansas (McJunkin et al., 2003). Since wild turkeys are a popular game bird, it is important to know what parasites inhabit these turkeys. This knowledge could also help wildlife management, and more specifically, wild turkey management as we continue to have interest in the wild turkey populations for both biodiversity and hunting. Additionally, domestic poultry share many parasites and diseases with wild turkeys and knowing the parasite communities of wild turkeys is essential to controlling disease in domestic poultry operations and preventing the spread of these diseases between wild and domestic populations. Since the wild turkey population in Colorado is still growing, there will be increasing transmission of parasites and diseases between wild turkeys and domestic poultry. This study will give us insight into which parasites are present in Colorado so that domestic poultry operations can take precautions to decrease the risk of transmission.

Materials and Methods

Turkey intestines were opportunistically collected from hunters during the hunting seasons. All samples were collected from birds that were killed by firearms, with the exception of one turkey that was obtained by bow hunting. None of the birds were killed exclusively for

this study. The benefit of collecting the intestinal tracts in this manner is that the samples came from around the state and represent a large area rather than one flock of turkeys (Oates et al., 2005). The disadvantage of this collection strategy is that all of the birds were handled by different people, the time until freezing may have varied, and if the samples were not frozen quickly, autolysis will have started to degrade the sample (Oates et al., 2005). The intestinal tracts were placed in plastic bags, labeled, and frozen as soon as possible after harvesting and remained frozen until examination. The collected sections included the crop, gizzard, small intestine, ceca, and large intestine, although the crop and gizzard were not present in seven samples. Each turkey's location, gender, and the date of harvest were recorded. Turkey intestines were collected from hunters during the fall 2012 season (September to October) and the spring 2013 season (April 13 – May 26). Overall, 25 intestines were obtained, 3 from the fall season and 22 from the spring season. One of the samples was not dissected due to the excessive amount of autolysis that had occurred.

The dissection methods and examination of the intestinal tract and parasites used in this study were adapted from an unpublished study by Donnelly (2005) and from Moore and Simberloff (1990). Once the intestinal tracts were thawed, the gizzard, small intestine, large intestine, and ceca were separated from each other. The small intestine was placed ventral side up so that it was possible to distinguish the left ceca from the right ceca. The small intestine was stretched with an 80-g spring to measure length in a manner that would be comparable across turkeys. Then, the small intestine was cut into ten equal sections, with section number one being the section that was most anterior. Each section was cut open lengthwise and the contents were washed through a 60-mm sieve. The contents and intestine were then be examined under a dissecting scope at 10X power and any parasites were removed and stored in 70% EtOH. The

large intestine and ceca were also cut open lengthwise and the same process was repeated. The gizzard was also examined for parasites by peeling away the inner keratin lining. Parasites found in the small intestine were identified and recorded according to the section number in which they were found. Cestodes were recorded in the section in which the scolex was found. Parasites found in any other part of the intestinal tract were recorded based on where they were found. The parasites were then identified by morphological characteristics.

Results

The 24 Colorado wild turkeys in this study were infected with three species of cestodes, two species of nematodes, one species of trematode, and one species of acanthocephalan (Table 3.1). Five of the 24 wild turkeys collected did not have any detectable enteric helminth parasites. The prevalences of the enteric helminths are reported in Table 3.1.

Table 3.1: Prevalence of the parasite species.

| Helminth Species | Prevalence (%) |
|----------------------------|----------------|
| Cestoda | |
| <i>Hymenolepis sp.</i> | 17/24 (70.8%) |
| <i>Imparmargo baileyi</i> | 2/24 (8.3%) |
| <i>Metroliasthes sp.</i> | 11/24 (45.8%) |
| Acanthocephala | |
| Unidentified sp. | 5/24 (20.8%) |
| Trematoda | |
| <i>Echinoparyphium sp.</i> | 2/24 (8.3%) |
| Nematoda | |
| <i>Heterakis sp.</i> | 2/24 (8.3%) |
| Unidentified sp. | 1/24 (4.2%) |

Cestodes

A total of 1,673 cestode scolices were collected from the Colorado wild turkeys. Prevalence was 79.2%. The number of cestodes per turkey ranged from zero to 559, with a mean

intensity of 88.05 (SD=125.76); the median intensity was 49 (Figure 3.1). Three cestode species were identified: *Hymenolepis sp.*, *Metroliasthes sp.*, and *Imparmargo baileyi*.

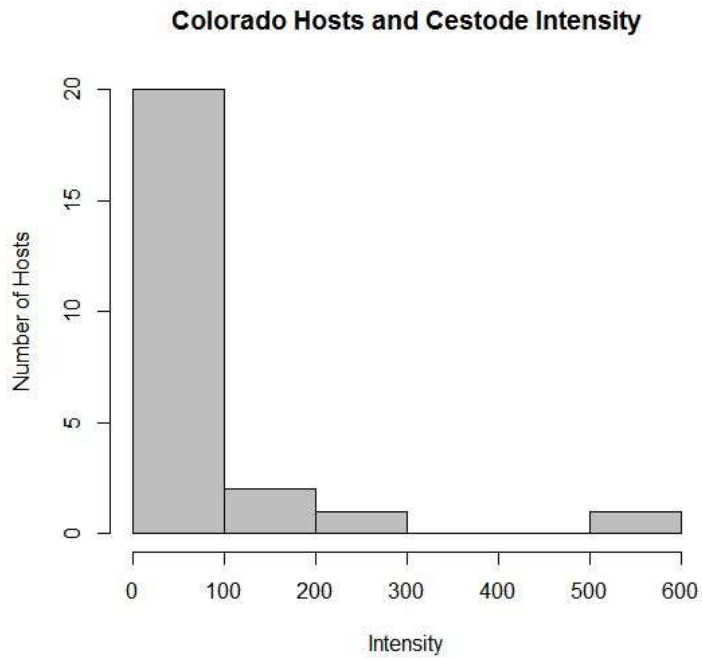


Figure 3.1: Intensity of cestodes in Colorado wild turkeys

Acanthocephalans

A total of 39 acanthocephalans were collected from the Colorado wild turkeys. Five out of the 24 turkeys were infected, yielding a prevalence of 20.8%. The number of acanthocephalans per turkey ranged from zero to 25. The mean intensity was 7.8 and the median intensity was 3.0 (Figure 3.2).

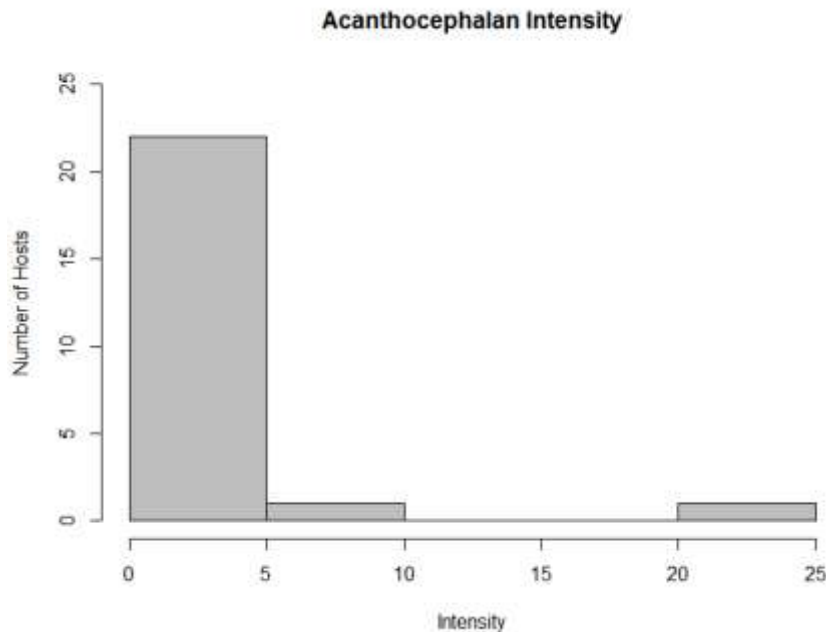


Figure 3.2: Acanthocephalan intensity in Colorado wild turkeys

Trematodes

A total of three trematodes were found in two wild turkey hosts and all were consistent with *Echinoparyphium sp.*, which have 45 collar spines (Lee et al., 1990). There was a prevalence of 2/24 (8.3%) and a mean intensity of 1.5.

Nematodes

A total of 47 nematodes were found. 46 of these nematodes were *Heterakis sp.* with a prevalence of 2/24 (8.3%). The range of *Heterakis sp.* found in a turkey was from zero to 45. The mean intensity was 23.5 nematodes. One partial specimen was found of a second species, and the partial segment measured 15 mm in length. Due to this extreme size difference, it was concluded that this is a different species, however it could not be identified due to it being an incomplete specimen.

Discussion

Cestodes

Hymenolepis sp., *Imparmargo baileyi*, and *Metroliasthes sp.* have all been identified previously in wild turkeys. *Hymenolepis sp.* have been identified in Alabama, Arkansas, Florida, Georgia, Illinois, Kentucky, Mississippi, Tennessee, and Virginia (Maxfield et al., 1963; Jackson et al., 1977; Hon et al., 1978; Castle and Christensen, 1984). *Metroliasthes sp.* have been identified in Alabama, Arkansas, Florida, Georgia, Illinois, Kansas, Kentucky, Louisiana, Mississippi, Oklahoma, Rhode Island, Tennessee, and Virginia (Self and Bouchard, 1950; Maxfield et al., 1963; Jackson et al., 1977; Hon et al., 1978; Castle and Christensen, 1984; Amr et al., 1988; McJunkin et al., 2003). *Imparmargo baileyi* has previously been reported in wild turkeys in Kansas and West Virginia (Davidson et al., 1974; Mcjunkin et al., 2003).

Acanthocephalans

Acanthocephalans are rarely reported in most studies of wild turkeys. When they are documented, acanthocephalan prevalence and intensity is low for wild turkey hosts. For example, a study in eastern Kansas found a prevalence of 2% in the spring and 0% in the fall (McJunkin et al., 2003). An unpublished study in Florida found a prevalence of 1/25 (4%) and this one host had an intensity of two acanthocephalans (Donnelly, 2005). In contrast to these studies, my findings show relatively high prevalence (20.8%) and mean intensity (7.8%) of acanthocephalans.

Additionally, the only acanthocephalan species to have been reported in wild turkeys is *Mediorhynchus grandis* (McJunkin et al., 2003). *Mediorhynchus sp.* was reported by Oates et al. (2005). The acanthocephalans reported in this study are not consistent with the characteristics of genus *Mediorhynchus*.

Trematodes

Trematodes have been commonly reported in studies of helminth species of wild turkey hosts. *Echinoparyphim sp.* have been found in wild turkeys previously in Alabama, Arkansas, Florida, Kansas, Louisiana, Tennessee, and Nebraska, (Maxfield et al., 1963; McJunkin et al., 2003; Oates et al., 2005).

Nematodes

Heterakis sp. is one of the most commonly reported nematodes from wild turkeys and is especially important because it is host to *Histomonas meleagridis* which causes blackhead disease in wild turkeys. Nematodes in general, including *Heterakis sp.*, are often reported at much higher prevalence in other studies of wild turkey hosts than reported here (Jackson et al., 1977; Hon et al., 1978; Castle and Christensen, 1984; McJunkin et al., 2003). The lower prevalence of nematodes in Colorado wild turkeys could be due to the relocation efforts. The reintroduced wild turkeys may have experienced parasite release when they escaped the nematodes that infected them before reintroductions. Additionally, because the origin of today's Colorado wild turkey is not known, it is possible that the nematodes that are found in other geographic areas such as the southeast are not able to survive the climate in Colorado. Therefore, the Colorado wild turkeys may have experienced parasite release.

Conclusion

Colorado wild turkeys are hosts to various gastrointestinal helminths, such as cestodes, trematodes, acanthocephalans, and nematodes. Colorado represents a unique parasite community for host wild turkeys, possibly due to the climate and/or due to the wild turkey reintroductions. In particular, the relatively high prevalence of acanthocephalans is intriguing since there is not a corresponding higher than normal prevalence of cestodes. If prevalence was influenced solely by

diet, it would be likely that cestode and acanthocephalan intensity would correlate since they are both obtained through insect intermediate hosts. However, my study does not show this pattern. More work is necessary in order to further understand how these helminth parasite communities affect the wild turkey populations and also to study the genetic origins of the wild turkeys in Colorado so that analyses can be conducted on parasite release and parasite spillback.

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CHAPTER 4: Comparison of Helminths of Wild Turkeys (*Meleagris gallopavo*) in Colorado, Florida, and New Zealand

Summary

The results from my study on helminth parasites of 24 Colorado wild turkeys are compared to previous unpublished data on 25 wild turkeys from Florida and 5 wild turkeys from New Zealand (Donnelly, 2005). To my knowledge, no comparative studies have examined the differences between the parasite communities of turkeys in the central part of the US and the east coast, where wild turkeys are endemic. A total of 7 helminth parasite species were found in wild turkeys from Colorado, 14 from wild turkeys in Florida, and 6 from wild turkeys in New Zealand. It is clear that the parasite communities of these three locations differ in terms of prevalence, abundance, and species richness.

Introduction

Wild turkeys are native to the United States, with their center of endemism in the southeast (Thornton et al., 2012). There is evidence that various Native American groups used wild turkeys as food sources, or used their feathers for decoration (Aldrich, 1967). The origins of the first domestic turkey are disputed, but by the 1530s, the domestic wild turkey was well established in Europe (Aldrich, 1967; Kennamer et al., 1967). In the United States in the 1920s, we saw a change to commercial domestic turkey operations from farm-raised turkeys (Kennamer et al., 1967). In the early 20th century, the wild turkey started experiencing severe declines due to overhunting and habitat loss (Mitchell et al., 2011). Historically, 39 states had wild turkey populations, and by the 1920s, only 18 of those states still had wild turkeys. Moreover, some of these 18 states had very small turkey populations as well. For example, the last wild turkey in Illinois was shot in 1905 (Smith, 2009). Around this time period, massive reintroduction efforts

started. Some of these were government operated, some were conducted by organizations and federations, and some turkeys were reintroduced by wild turkey enthusiasts eager to help wild turkey populations. For these reasons, the reintroduction and relocation information is not always well documented, especially in some states such as Colorado. One of these groups is the National Wild Turkey Federation, who strive to conserve the wild turkey so that it has population sizes large enough to sustain hunting. Across the United States, the current range of the wild turkey now extends further than the historic range (Mock et al., 2001; Oates et al., 2005).

Wild turkeys have now been introduced all over the world, and similarly domestic turkeys are found in many different locations. This history of the wild turkey allows for interesting comparisons. This study looks at 3 locations that have different histories. First, my study addressed Colorado wild turkeys; these turkeys lived in Colorado historically, experienced local extinctions, and then were reintroduced. Second, an unpublished study addressed Florida wild turkeys; these turkeys are endemic to Florida. Lastly, an unpublished study addressed New Zealand wild turkeys; these turkeys were relatively recently introduced, around 1890 (Oliver, 1955; Falla et al., 1967).

Even though it is difficult to make direct comparisons due to the vastly different geographies, climates, and ecosystems of these three areas, how the different histories of the host turkeys could influence the parasite communities is still intriguing. Florida wild turkeys have had a long time to interact with their parasites. Colorado turkeys could have been reintroduced, bringing new parasites, or perhaps they picked up their parasites from the other native host species. They may have lost some species as well. Wild turkeys in New Zealand also could have parasites from their previous location, or obtained new parasite species from native hosts.

Turkeys also are non-migratory birds and therefore they will not pick up parasites from different locations during the different seasons.

Methods

The data from the Florida wild turkeys were obtained from an unpublished thesis by Donnelly (2005). In that study, wild turkey intestines from Florida were collected from 25 wild turkeys that were killed by hunters in 1996, 1997, and 1998. Five wild turkeys were collected by hunters in New Zealand. For comparison, 24 wild turkey intestines were collected in Colorado in 2012 and 2013. In all cases, the intestinal tracts were frozen as soon as possible after harvesting and remained frozen until examination. Each turkey's location, gender, and the date of harvest were recorded.

The materials and methods for dissection and examination of the intestinal tract and parasites were adapted from Moore and Simberloff (1990). Once the intestinal tracts were thawed, the gizzard, small intestine, large intestine, and ceca were separated from each other. The small intestine was stretched with an 80-g spring to measure length. The small intestine was cut into ten equal sections. Each section was cut open lengthwise and the contents were washed through a 60-mm sieve. The contents and intestine were then examined under a dissecting scope at 10X power and any parasites were removed and stored in 70% EtOH. The large intestine and ceca were also cut open lengthwise and examined in the same manner. The gizzard was examined for parasites by peeling away the inner keratin lining. Parasites found in the small intestine were identified and recorded according to the section number in which they were found. Cestodes were recorded in the section in which the scolex was found. Parasites found in any other part of the intestinal tract were recorded based on where they were found.

Results and Discussion

Table 4.1: Helminth species reported in wild turkey hosts from Colorado, Florida, and New Zealand

| | Colorado | Florida | New Zealand |
|----------------------------------|----------|---------|-------------|
| Sample Size | 24 | 25 | 5 |
| Helminth sp. richness | 7 | 14 | 6 |
| Prevalence of: | | | |
| <i>Hymenolepis sp.</i> | 70.8% | 56% | - |
| <i>Imparmargo baileyi</i> | 8.3% | - | - |
| <i>Metroliasthes sp.</i> | 45.8% | 84% | - |
| <i>Raillietina georgiensis</i> | - | 84% | 40% |
| <i>Raillietina ransomi</i> | - | 52% | - |
| <i>Raillietina williamsi</i> | - | 60% | - |
| <i>Aonchotheca bursata</i> | - | 4% | 40% |
| <i>Aonchotheca caudinflata</i> | - | 4% | 100% |
| <i>Ascarida dissimilis</i> | - | 92% | - |
| <i>Baruscapillaria obsignata</i> | - | - | 60% |
| <i>Capillaria sp.</i> | - | - | 100% |
| <i>Dispharynx nasuta</i> | - | 8% | - |
| <i>Gongylonema ingluvicola</i> | - | 4% | - |
| <i>Heterakis sp.</i> | 8.3% | 100% | - |
| <i>Trichostrongylus sp.</i> | - | 20% | 60% |
| Acanthocephala | 20.8% | 4% | - |
| <i>Echinoparyphium sp.</i> | 8.3% | - | - |
| Trematoda (liver) | - | 20% | - |

*One species of nematode from Colorado was unidentified due to a partial specimen

Three species of cestodes (*Hymenolepis sp.*, *Imparmargo baileyi*, and *Metroliasthes sp.*) were reported from Colorado wild turkeys. Five species of cestodes (*Hymenolepis sp.*, *Metroliasthes sp.*, *Raillietina georgiensis*, *Raillietina ransomi*, and *Raillietina williamsi*) were reported from Florida wild turkeys. The New Zealand data represent such a small sample size that it is difficult to draw conclusions, however there are still parasite species represented that can be compared to the other locations. Only one species of cestode (*Raillietina georgiensis*) was reported from wild turkeys in New Zealand, possibly due to this small sample size, or possibly due to parasite release (Table 4.1).

Two species of nematodes (*Heterakis sp.* and an unidentifiable partial specimen) were reported from wild turkeys in Colorado. Both of these species were found in the caeca. For the other species, only one specimen was found and it was a partial specimen and therefore could not be identified. The piece that was found was almost twice the length of the other nematodes found, thus leading to the conclusion that it is a different, if unidentifiable species. In Florida wild turkeys, seven species of nematodes were reported (*Aonchotheca bursata*, *Aonchotheca caudinflata*, *Ascarida dissimilis*, *Dispharynx nasuta*, *Gongylonema ingluvicola*, *Heterakis gallinarum*, and *Trichostrongylus sp.*). Five species of nematodes (*Aonchotheca bursata*, *Aonchotheca caudinflata*, *Baruscapillaria obsignata*, *Capillaria sp.*, and *Trichostrongylus sp.*) were found in wild turkeys from New Zealand.

Acanthocephalans were found in Colorado and Florida, but not in New Zealand. The acanthocephalans from Colorado are yet to be identified, but are not consistent with the genus *Mediorhynchus*, which is the only genus of acanthocephalans that has been reported in the literature. In the unpublished Florida study, the acanthocephalans were identified as *Plagiorhynchus cylindraceus*.

Trematodes were found in both Colorado and Florida. However, *Echinoparyphium sp.* was found in the intestines of wild turkeys while an unidentified trematode was found in the liver of wild turkeys in Florida.

Conclusion

These differing geographic locations have different helminth communities in the wild turkey hosts. These differences could be attributed to many factors including climate, other hosts, and history of introduction/reintroduction. One major trend in biogeography that may help to explain these differences is that more species are found near the equator. More than the three

studies examined here would be needed to truly examine whether parasite species richness of wild turkeys corresponds to latitude, but based on these studies, parasite species of wild turkey hosts could demonstrate this trend. Understanding the helminth communities of wild turkeys in different locations is important for wild turkey management, reintroduction efforts, as well as for domestic poultry operations.

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CHAPTER 5: Using Online Content to Study Behavioral Biology

Summary

Viewing animal behavior in the wild is time consuming, can be costly, and often yields few results compared to the time required. This assignment encourages students to explore animal behavior through online videos while developing research and critical thinking skills. The approach allows students to get a field-like experience from a lecture-based class and enhances knowledge about behavior of animals beyond the students' geographic area. This assignment is appropriate for both college and high school biology classes that cover animal behavior, ecology, or conservation.

Key Words

Animal behavior; video; critical thinking; research

Behavioral biology is a rewarding field, and one that many students find fascinating. As the proliferation of animal behavior shows on television attests, it has broad appeal; it may even be a gateway to biology for students who otherwise may not be interested. Unfortunately, it is a difficult topic for a class to study in the field for a variety of reasons. Even if transportation to field sites were not expensive in terms of time, money, and liability issues, and even if expanding class sizes did not compromise field observation, biologists are well aware that animals seldom show up and behave on cue, nor do their activity cycles match laboratory schedules. Courses on campus may resort to local geese, ducks, and squirrels, but these animals may be semi-domesticated, and even this limited assortment may not be available on some urban campuses.

In contrast, there is a wealth of video recordings of animals online. Many of these are videos of cute kittens or amusing dogs, but there are countless recordings of animals performing

behaviors in their natural habitats. These videos are taken by professionals and nature enthusiasts alike. In general, web content is increasingly integrated into classrooms to benefit the students' learning, engage students, and share with the students the vast resources that are available to them online. The study of animal behavior stands to benefit greatly from this trend.

We have developed an online assignment involving the use of existing videos for a college animal-behavior course. This assignment can act as a substitute for a lab portion of a class, and it can easily be modified to suit high school biology instruction.

Goals/Objectives

One of the main objectives of this assignment is to expose students to a variety of animal behaviors. Access to online videos is both significantly cheaper than field observation and much more efficient. An hour spent watching and asking questions about animal behavior videos is likely to engage the beginning student much more than an hour spent in the field hoping to see even one animal behave.

Another objective of this assignment is to hone skills that are necessary in the college environment as well as in future jobs. Most students have ample experience in searching the internet and therefore this assignment allows them to use skills that they have already acquired to enhance other skill sets such as library research, critical thinking, and writing. In small classes, it can also involve oral presentation.

The use of videos allows students to experience a field-type exercise in a lecture-based class. It also gives students the ability to examine the behavior of non-domestic animals from all over the world, that are active at all times of day (and night), and encourages enthusiasm and participation through the use of internet resources. For large classes, this exercise allows an

added measure of flexibility as students can choose an animal or topic of special interest for further scrutiny.

Because this exercise is organized around the core principles of animal behavior, students will also benefit from this assignment by exploring those fundamentals through an exciting source. The Nobel Laureate, Niko Tinbergen (1963) came up with a set of four questions to better understand behavior at various levels. Since that time, these questions have provided the framework for animal behavior (for a recent explication, see Bateson & Laland, 2014):

- What is the cause (mechanism) of the behavior?
- How does a behavior develop?
- What is the survival value (adaptive significance) of the behavior?
- How did the behavior evolve from ancestral forms?

Using these questions, internet videos, and library resources, students can create and test hypotheses about the behaviors that they see online.

Materials

There are few materials needed for this assignment, and most of these materials are readily available to most students.

- Access to the Internet and websites such as www.youtube.com and www.arkive.org.
- Access to peer-reviewed journal articles so that they can substantiate their hypotheses with data from the literature (often available through the online databases provided by the school). If journal articles are not available, access to books and major online reference works can be helpful (e.g., Breed & Moore, 2010).
- An online discussion board, such as that found on many classroom websites.

Implementation of the Assignment

When introducing the assignment, the instructor should communicate the goals and expectations to the students (see Table 1). For example, instructors should explain that only videos of wild animals will be accepted. The assignment occurs in four stages so that students will not attempt to finish it in one evening, and so that other students can participate in online discussion. We summarize the stages below.

1. **View and post video.** The first task for students is to start viewing videos online. During this process, students must think about and ask Tinbergen's four questions about the behaviors that they are viewing. If a student is interested in one question more than others, s/he may ask how the videos fits their question; if a student is interested in a certain set of organisms, then how do the available videos pair with specific questions? Once the student has surveyed the videos and has an idea about the kinds of videos on offer and which ones are interesting, s/he should choose a video and post it onto the discussion board. A brief, approximately two-sentence description of the video should be included with the link to ensure that no other students use the same video. In a large college class, the students may be given a list of topics based on textbook chapters or syllabus areas. The video can then be categorized by the topic.

2. **Ask Tinbergen's Question, develop hypothesis.** Once the video has been posted, each student will need to ask one of Tinbergen's four questions about the video s/he has posted and develop a hypothesis in response to that question.

3. **Support or refine hypothesis.** Students should use peer-reviewed journals or other credible sources to support their hypotheses. If they do not find support for their hypotheses in the literature, they should refine their hypotheses and include support for the refined hypotheses. In all cases, they should use credible sources, citing references.

4. Critique hypotheses.

a. In large classes, after completing stages 1-3 for their own videos, students are encouraged to look through the videos and comments of their classmates. They should critically examine these and decide whether they have different ideas or if they agree with what was said. Students are asked to comment on four videos that their classmates have posted to facilitate a discussion. They should clearly state whether they agree or disagree with the hypothesis and include a new citation to support their comments.

b. In small classes, students may present their videos, hypotheses, and discussion to the class. This can be used as a springboard for lively class discussion.

Assessment

Following the guidelines of this assignment is important and students should be graded on all aspects of the assignment (see Table 5.1). Instructors may want to set word-counts, especially if the class is large. The assignment write-up should be fairly brief so that other students can read many of them and choose the ones on which they want to comment.

Table 5.1: Criteria for assignment evaluation

| |
|--|
| Students will be graded on the following criteria: |
| 1. Categorization of the video - Categorize the video into one of the topics provided in the assignment instructions |
| 2. Description of the video - Briefly (2 sentences) describe the video and provide a URL to the video so that other students can watch it |
| 3. Tinbergen's question - Ask one of Tinbergen's four questions, applying it to the selected video |
| 4. Hypothesis - Formulate a hypothesis that provides a possible answer to Tinbergen's question (item 3) |
| 5. Support for hypothesis - Citing credible sources in all three instances, do one of the following: a.) provide support for the hypothesis (item 4), b.) refine the hypothesis, or c.) refute the hypothesis and put forward a different one |
| 6. References - Be sure that cited references are appropriate and reliable (e.g. from peer-reviewed journals, major reference works, etc.) - Cite references in the format indicated in the assignment instructions - Provide at least two references |
| 7. Spelling, grammar, and format - Provide information in a clear, concise manner, paying attention to spelling and grammar. |

Assignment Flexibility

This assignment was initially developed for a junior-level animal behavior course at Colorado State University in Fort Collins, CO. This class is a lecture class only and enrolls up to 150 students. The online discussion board allowed the students to view each other's responses on their own time and to participate in discussions about the videos. We have also adapted this assignment to fit the same class when it is taught in the summer and there are about 15-20

students. In this case, the students created a PowerPoint presentation of their video, Tinbergen's question, their hypothesis, and their support from the literature. This presentation then led to a class discussion about how Tinbergen's questions can be applied to the video and other hypothesis about the behavior. In short, this assignment can easily be adapted to fit any size class and could even work for an entirely online classroom. This assignment can also be adapted for high school students who are studying organismal biology.

Student Comments

Below are some selected student comments about this assignment:

- “I did like this assignment because it was an unconventional way of applying the things we were learning in class. I liked it because it was also very relevant.”
- “It was cool to see all the different videos that the other students found and watch them through the lens of animal behavior.”
- “It required me to analyze a behavior that I found interesting and apply class concepts and additional research to understand the behavior more.”
- “This assignment was fun because I enjoyed spending hours watching animal videos. This assignment also helped me understand the material in real life experiences, and now I cannot watch an animal doing any activity without thinking of one of Tinbergen's questions.”
- “This assignment was a great opportunity to take what we've been discussing in class and apply to something we have access to in the real world, similar to what one might find in a class with a lab. It was a simple, straightforward and engaging assignment.”

- “I liked it because I was a little excited to see other people’s comments on my video. Comments were definitely my favorite because it also meant I could watch videos of other animals. Like the howling mouse, this was cool!”

Acknowledgements

We thank all of the students who have participated in this assignment and given us feedback in order to shape this assignment into what it is today. We also thank Dr. Randy Moore and Ms. Kayla Brown for their helpful comments on this manuscript.

References

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APPENDIX 1: Host Turkey, Hunter, Location Collected, Year Collected, and Small Intestine Length

| Turkey | Hunter/Donator | Location | Year | SI Length |
|---------------|------------------------------|--|-------------|------------------|
| A | Broox Boze | Julesburg | 2012 | 204 cm |
| B | Broox Boze | Julesburg | Unknown | 235 cm |
| C | Russ Means | Colorado River | 2013 | 218 cm |
| D | Ryan Urie | Sterling | 2013 | 180 cm |
| E | Ryan Urie | Trinidad | 2013 | 211 cm |
| F | Ryan Urie | Trinidad | 2013 | 220 cm |
| G | Tom Haverty | Buckhorn | 2013 | -- |
| H | Linus Leppink | Unit 851 | 2013 | 200 cm |
| I | Linus Leppink | Unit 851 | 2013 | 193 cm |
| J | Linus Leppink | Unit 130 | 2013 | 210 cm |
| K | Linus Leppink | Unit 130 | 2013 | 209 cm |
| L | Linus Leppink | Unit 130 | 2013 | 182 cm |
| M | Linus Leppink | Unit 130 | 2013 | 165 cm |
| N | Keith Ewald | South Platte River near Brush, Colorado, Unit 96 | 2013 | 180 cm |
| O | Ed Gorman | Unit 96 | 2013 | 218 cm |
| P | Dawson Swanson via Ed | Unit 96 | 2013 | 172 cm |
| Q | Jeff Mekeldore via Ed Gorman | Unit 91 | 2012 | 225 cm |
| R | Ed Gorman | Unit 96 | 2013 | 172 cm |
| S | Ed Gorman | Unit 102 | 2013 | 210 cm |
| T | Ed Gorman | Unit 91 | 2013 | 230 cm |
| U | Ed Gorman | Unit 91 | 2013 | 228 cm |
| V | Joe Cugliat | Unit 91, area 11 east | 2013 | 210 cm |
| W | Ed Gorman | NW corner of Angustora Reservoir | 2013 | 210 cm |
| X | Ed Gorman | 96 | Unknown | 189 cm |
| Y | Ed Gorman | Unknown | Unknown | 183 cm |