# *SARCOPTES SCABIEI* IN THE AMERICAN BLACK BEAR *(URSUS AMERICANUS):* EFFECTS OF MITE BURDENS AND LANDSCAPE FACTORS ON DISEASE

by

JILLIAN ROSE BROADHURST

(Under the Direction of Michael J. Yabsley)

## ABSTRACT

Mange is a dermatological syndrome affecting mammalian species worldwide. In wild populations, it can contribute to significant morbidity and mortality. *Sarcoptes scabiei,* the mite causing sarcoptic mange, impacts over 150 mammals, including humans. *S. scabiei* has been implicated in disease events across many wildlife species, but only recently emerged as a health threat to North American black bear (*Ursus americanus*) populations for reasons not well understood. This work intended to add to the exploration of sarcoptic mange impacts on black bears. The first chapter contains a literature review outlining mange in wildlife, particularly focusing on *S. scabiei*. The second chapter evaluates impacts of *S. scabiei* mite burdens on clinical disease outcomes. The third chapter analyzes spatial trends in sarcoptic mange reports. Lastly, the final chapter offers concluding remarks and implications of this work. These results will improve understanding of this disease challenge, bolstering conservation and management efforts.

INDEX WORDS: *Sarcoptes*, sarcoptic mange, black bear, scabies, wildlife health

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JILLIAN ROSE BROADHURST

B.S., The University of New Hampshire, 2021

A Thesis Submitted to the Graduate Faculty of The University of Georgia in Partial Fulfillment of the Requirements for the Degree

MASTER OF SCIENCE

ATHENS, GEORGIA

2025

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|---|---|
| Major Professor: | Michael J. Yabsley |
| Committee: | Michel T. Kohl |
| | Ellen Haynes |

Electronic Version Approved:

Ron Walcott
Vice Provost for Graduate Education and Dean of the Graduate School
The University of Georgia
August 2025

# DEDICATION

I dedicate this work to the many four-legged creatures I have had the pleasure of knowing. From my beloved pets over the years, to all those I helped treat in the veterinary medicine world, and every one I have worked with in the wild; let this thesis and the rest of my life’s work be for you.

Alongside these sentient beings, I also dedicate this work to the White Mountains of New Hampshire, the first wild space to inspire my love of the natural world and set my heart alight.

# ACKNOWLEDGEMENTS

I would like to thank my advisor, Michael Yabsley, for all of the support, laughter, and wonderful opportunities. Learning under your wing has allowed me to grow immensely in this field over the last couple of years, and I am grateful for you taking a chance on the random girl you met over zoom halfway across the country!

Thanks to my committee members, Michel Kohl and Ellen Haynes, for fielding my endless questions and for offering all your advice and wisdom. Both of you, and Michael, have all shown me that we can be wildlife professionals and still be real people at the same time. I would also like to thank my past advisors and educators, especially Drew Conroy at UNH, for setting me on this path-I would not be here writing this without your mentorship and investment in my growth.

Thank you to my SCWDS and Warnell family for your friendship and support both inside and outside of the lab. It is not lost on me how lucky I am to be here, and I am thankful every day that I ended up getting to work with such wonderful people. There is not a better place that I could have come to conduct this work.

An enormous thank you is owed to my friends near and far, without whom I would be nowhere. I don’t know what I did to get such truly amazing people in my life-some of whom are sitting next to me and keeping me sane as I write this. I am forever grateful for all of you.

Finally, I want to express the greatest gratitude to my family for their truly infinite love and support. To Lukie, it has been the greatest blessing watching you grow up. I can’t wait to see what you do next. Lindsey, I’m so happy that I get to be your day one. You will always be a

built-in best friend for me, and I am so grateful for that. Mom, thanks for showing me what unconditional love is, and for going to the ends of the earth for me…...and also for making sure I wake up on time. Dad, thank you for always picking me up when I'm down, talking me through every obstacle, and for being the one to help me find my passion in the outdoors. I can confidently say that none of this would have been possible without either of you, Mom and Dad. Also, obviously I have to give the biggest shout out to my cat Sheldon-thank you for being my best buddy, my source of happiness and joy every day, and for loving me so much. You have stuck by my side and been the one constant through at least six moves and three states. Adopting you has saved my life-thank you for choosing me.

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# CHAPTER I

# INTRODUCTION AND LITERATURE REVIEW

## Introduction: Mange in Wildlife

Mange is a skin condition caused by the infestation of parasitic mites that can impact humans as well as a variety of domestic and wild animals. It is a global issue for numerous mammalian species, leading to both individual morbidity and population-level impacts. While clinical manifestations can be variable depending on the host and mite species associated with the infestation, mange is characterized by abnormalities in the epidermal layer of the skin, including alopecia, scabbing, hyperkeratosis and crusting, extreme pruritus, hyperemia and erythema. Mites serving as the etiologic agent of mange complicates the study of this important disease problem, as these ectoparasites represent one of the most taxonomically diverse animal groups. Well over 50,000 species of mites have been documented, with more than 250 of these known to cause disease in mammalian hosts and at least 50 mite species known to cause mange (Escobar et al., 2022; Mullen & OConnor, 2019). Many of these mites remain understudied, complicating our understanding of the pathogenesis of mange in wildlife.

Mange mites pose significant threats to animal health and have been documented to parasitize nearly all vertebrate hosts (Mullen and OConnor, 2019). Particularly notable mite species in wildlife include: *Notoedres* spp., known to primarily infest felids, rats, rabbits, and squirrels (Abd El-Ghany, 2022; Grunert et al., 2022; Marcondes, 2017; Riley et al., 2007); *Psoroptes* spp., infesting ungulates such as sheep and deer, rabbits, and bovids (Boyce & Brown, 1991); *Chorioptes* spp., mainly affecting ruminants including bovids, gazelles, moose (*Alces*

*alces*), elk (*Cervus canadensis*), vicuñas (*Lama vicugna*), guanacos (*Lama glama guanicoe),* and serows (Kadulski, 1996; Takahashi et al., 2001; Mullen & OConnor, 2019; Zahler et al., 2001), but also rabbits, badgers, a captive panda bear (*Ailuropoda melanoleuca*), captive coatis, and a wild American black bear (*Ursus americanus*) (Bochkov et al., 2014; Fain & Leclerc, 1975; Klinger et al., 2021; Niedringhaus et al., 2021); *Demodex* spp., parasitizing an extremely wide variety of taxa across nine orders (Izdebska & Rolbiecki, 2020); *Ursicoptes* spp., currently known to infest bears and raccoons (*Procyon lotor*) (Fain and Johnston, 1970; Broadhurst et al., 2025; Fain & Wilson, 1979); other members of the Rhyncoptidae family, which predominantly parasitize primates (Mullen & OConnor, 2019); *Otodectes cynotis* in felids (Degiorgis et al., 2001; Marcondes, 2017); mites in the Knemidokoptinae subfamily, the causative agent of knemidokoptic mange in numerous avian species (Marcondes, 2017; Rivera Reyes et al., 2025); mites of the Psorergatidae family, parasitizing rodents, shrews, bats, ungulates, primates, rabbits, and mustelids (Giesen, 1990; Izdebska & Fryderyk, 2012); mites of the Cheyletiella family, parasitic on rabbits, foxes and badgers (Smiley, 1970); and, arguably of most importance due to its prolific host and geographic distribution, *Sarcoptes scabiei*, the mite species implicated in cases of sarcoptic mange. In the American black bear, four mite species are known to cause mange: *Demodex ursi* (Desch, 1995; Foster et al., 1998); a *Chorioptes* sp. (Niedringhaus et al., 2021); *Ursicoptes americanus* (Broadhurst et al., 2025); and *Sarcoptes scabiei* (Schmitt et al., 1987; Niedringhaus et al., 2019d). Due to its larger prevalence and greater propensity to impact bear population health, *S. scabiei* will remain the primary focus of the following review and research.

*Sarcoptes scabiei*, the causative agent of scabies in humans and sarcoptic mange in animals, has long been identified as an indiscriminate and highly generalized ectoparasite affecting a diverse range of mammalian species across a wide geographical distribution (Andrews, 1983; Escobar et al., 2022; Niedringhaus et al., 2019a). Scabies is one of the earliest recorded diseases, even included in biblical references (Currier et al., 2011; Roncalli, 1987). With cases occurring globally across numerous taxonomic groups, sarcoptic mange has great potential to threaten conservation efforts and overall wildlife health.

An arachnid species of the order Sarcoptiformes and family Sarcoptidae, *S. scabiei* is a burrowing mite that creates tunnels to migrate deep into the epidermal layer of the host's skin (Arlian, 1989). This burrowing behavior typically results in mild to severe dermatological disease. Common clinical manifestations in the host include hyperkeratosis and crusting of the skin, erythema, alopecia, and pruritus (Arlian & Morgan, 2017; Escobar et al., 2022; Niedringhaus et al., 2019a). The initial dermal trauma inflicted by the mite is often exacerbated by the host's immune response to the mite's antigenic material (Niedringhaus et al., 2019a; Tiffin et al., 2020). This may result in a Type I (immediate) hypersensitivity response, characterized by rapid white blood cell hyperplasia, or a Type IV (delayed) hypersensitivity response, with the proliferation of T-lymphocytes (Little et al., 1998). The type of immune response observed, which is largely dependent upon host species and individual immunocompetence, can influence subsequent clinical signs and disease severity. In severe cases, these initial skin lesions can result in secondary bacterial and fungal infection, dehydration, emaciation, anorexia, and death (Niedringhaus et al., 2019a). Treatment options include acaricides such as ivermectin, afoxolaner, fluralaner, amitraz, moxidectin, selamectin and permethrin (Beugnet et al., 2016; Currier et al., 2011; Curtis, 2004). While these can improve clinical signs in some individuals and species, their use in wild populations is controversial (Niedringhaus et al., 2019a; Rowe et al., 2019).

In North America, canids such as coyotes (*Canis latrans*), wolves and foxes are disproportionately affected (Niedringhaus et al., 2019a). Although there are no reports of sarcoptic mange in black bears before the late 1980s, *S. scabiei* has emerged as a threat to North American bear populations over the last few decades, causing many mortalities and potentially population health declines in some regions (Niedringhaus et al., 2019d). The reasons for this recent emergence, however, are not well understood. Many factors have been theorized, including anthropogenic disturbance, geographic spread of the parasite, spatial population dynamics of the host, or host and parasite genetic characteristics (Niedringhaus et al., 2019d). Additionally, it is thought that host risk factors may predispose specific bear populations to severe mange, such as the presence of co-infections, increased mite burdens, or the likelihood of increased inter- and intraspecies interactions (Niedringhaus et al., 2019b; 2019d). Due to the knowledge gaps surrounding this mite species and its potential to impact black bear conservation, a bolstered understanding of the parasite and its host impacts is needed.

## **Literature Review: Sarcoptic Mange in Wildlife**

### SARCOPTES SCABIEI

#### *Mite Phylogeny and Classification*

Mites are small animals of the phylum Arthropoda, and further classified into the subphylum Chelicerata; this group is characterized by their chelicerae (feeding appendages), pedipalps (sensory appendages), and four walking appendages (Sharma & Gavish-Regev, 2025). Mites are typically further defined by their two distinct body regions: the prosoma, or anterior body region, contains the eyes and appendages, while the opisthosoma, or the posterior body region, contains major organs and is the site of gas exchange (Sharma & Gavish-Regev, 2025;

Walter & Proctor, 2013). However, mites of the class Arachnida (subclass Acari; contains > 55,000 species) differ slightly from other chelicerates and arachnids in that they are structured by an anterior gnathosoma, or feeding region akin to the head, and a posterior idiosoma (Walter & Proctor, 2013). The superorder Acariformes and order Sarcoptiformes contain the Sarcoptidae family, which comprises of over 100 species across three subfamilies (Arlian & Morgan, 2017; Bochkov, 2010). The subfamily Sarcoptinae holds four genera including *Sarcoptes*, with *S. scabiei* being the only species in that genus (Arlian & Morgan, 2017).

### *Morphology*

*S. scabiei* is characteristically oval in shape with a ventrally flattened and dorsally convex body (Arlian, 1989; Arlian & Morgan, 2017; Marchiondo & Endris, 2019). Key distinguishing features include cuticular spines and striations, or denticles, on the mid-dorsal idiosoma (body), club-like setae on the posterior dorsal idiosoma, and a terminal anus (Figure 1.1), (Pence & Ueckermann, 2002; Arlian, 1989; Arlian & Morgan, 2017; Fain, 1968; Pence et al., 1975; Wall & Shearer, 2001). Adults have eight legs, while larvae have six. Legs are stout and do not extend far past the idiosoma (Figure 1.1). In adults, the first two pairs of legs on the anterior-most region are positioned at the end of the idiosoma and extend past the body, while the two posterior pairs of legs do not extend past the idiosoma (Niedringhaus et al., 2019a). Empodial claws and a sucker-like pulvillus are present on the pretarsi of first two pairs of legs (Figure 1.1). The latter pairs of legs in the female and the third pair in the male end in long setae (Wall & Shearer, 2001). Females are significantly larger than their male counterparts, measuring 0.3-0.45 mm in length and 0.25-0.35 mm in width. Eggs are oval and measure 0.15-0.20 mm. Adult males are roughly half the size of the mature female and measure 0.20-0.24 mm in length (Marchiondo &

Endris, 2019; Yabsley et al., 2025). Initial descriptions were written by Fain (1968) with additional detail.

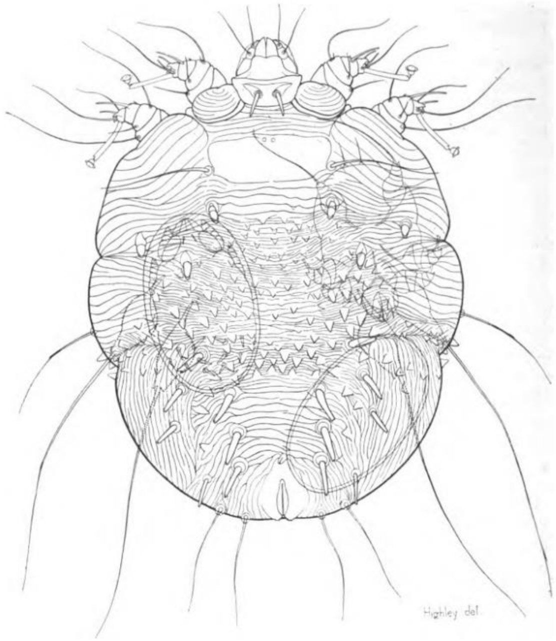
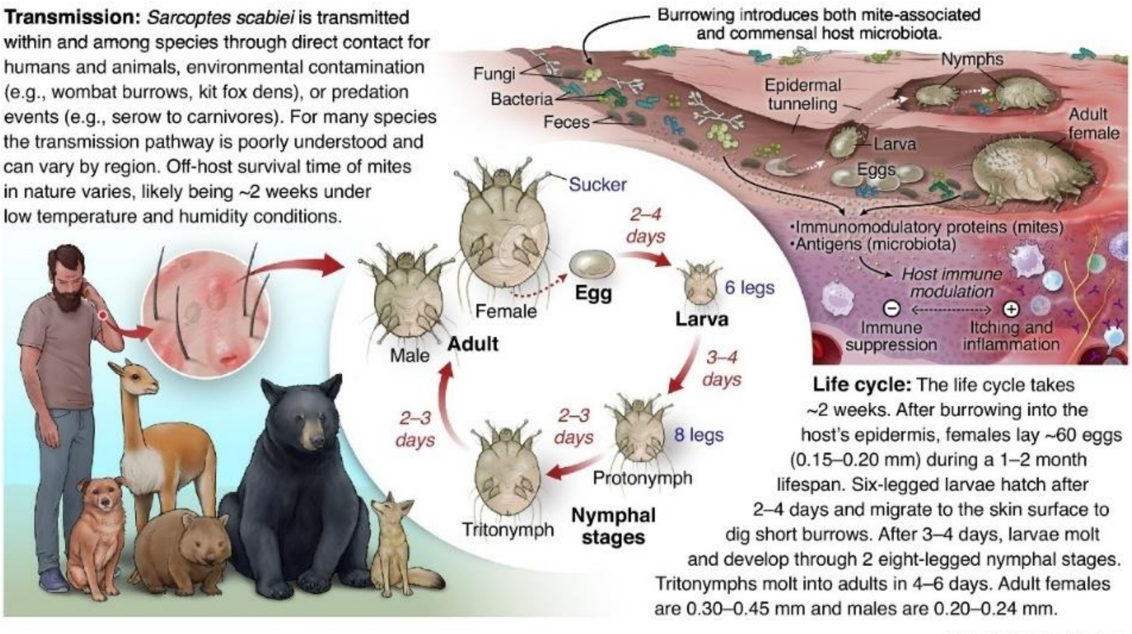


Figure 1.1. Dorsal view of a gravid adult female *Sarcoptes scabiei* mite showing several morphological features. (From Hirst, 1922).

*Life Cycle*

The ability of *S. scabiei* to colonize the host so effectively is owed in part to the parasite's ability to complete its full life cycle in about two weeks. This rapid maturation and proliferation leads to a quick onset of infestation and disease in the host. Adult mites burrow into the epidermal layer of skin and mate, then females deposit eggs (Figure 1.2), (Currie & McCarthy, 2010). Over her lifetime, the female can produce about 50-60 eggs (Arlian & Morgan, 2017). Eggs hatch within two to four days and give rise to larvae (Arlian & Vyszenski-Moher, 1988;

Currie & McCarthy, 2010; Yabsley et al., 2025). Three to five days later, larvae undergo their first molt to the protonymphal stage (Arlian & Morgan, 2017; Arlian & Vyszenski-Moher, 1988). Two to three days later, protonymphs molt and become tritonymphs; tritonymphs then undergo their final molt to reach their adult stage after an additional two to three days (Figure 1.2), (Arlian, 1989; Arlian & Morgan, 2017; Arlian & Vyszenski-Moher, 1988; Yabsley et al., 2025). Slight variations in developmental times have been observed, likely due to variations among in vivo conditions and observational protocols, and/or varying hosts (Arlian & Morgan, 2017). Although many individuals migrate back to the skin surface and dig new burrows during development, it is also possible for mites to complete the entire developmental process without exiting the initial burrow (Arlian & Vyszenski-Moher, 1988).



**Transmission:** *Sarcoptes scabiei* is transmitted within and among species through direct contact for humans and animals, environmental contamination (e.g., wombat burrows, kit fox dens), or predation events (e.g., serow to carnivores). For many species the transmission pathway is poorly understood and can vary by region. Off-host survival time of mites in nature varies, likely being ~2 weeks under low temperature and humidity conditions.

Burrowing introduces both mite-associated and commensal host microbiota.

•Immunomodulatory proteins (mites)
•Antigens (microbiota)

**Life cycle:** The life cycle takes ~2 weeks. After burrowing into the host's epidermis, females lay ~60 eggs (0.15–0.20 mm) during a 1–2 month lifespan. Six-legged larvae hatch after 2–4 days and migrate to the skin surface to dig short burrows. After 3–4 days, larvae molt and develop through 2 eight-legged nymphal stages. Tritonymphs molt into adults in 4–6 days. Adult females are 0.30–0.45 mm and males are 0.20–0.24 mm.

Trends in Parasitology

Figure 1.2. Depiction of the burrowing behavior and life cycle of *Sarcoptes scabiei.* (From Yabsley et al., 2025).

### *Transmission*

The transmission dynamics of sarcoptic mange in black bears also warrants further study. *Sarcoptes scabiei* is thought to spread mainly via direct contact between hosts, but indirect transmission via fomites or shared habitat spaces (i.e., denning sites) is also likely to play a role (Andrews, 1983; Arlian & Morgan, 2017; Browne et al., 2022). The importance of different transmission mechanisms in sustaining endemicity in wildlife populations is variable and largely dependent upon the ecology of the host species (Niedringhaus et al., 2019a). Population density is a widely recognized factor influencing the rate of *S. scabiei* spread via direct transmission, although frequency-dependent transmission dynamics have been shown to be more relevant in some populations (Browne et al., 2022; Devenish-Nelson et al., 2014; Niedringhaus et al., 2019a). With the propensity for increased inter- and intraspecies contact to facilitate spread, it is possible that a density-dependent relationship exists among affected bears.

Indirect transmission routes must be equally considered, especially for a relatively solitary species such as the black bear. The extent to which these methods facilitate spread, however, is questionable and highly variable depending upon the species and environmental conditions at hand (Browne et al., 2022). In wombats, for example, shared burrow spaces are considered a critical reservoir for mites in populations suffering from outbreaks (Martin et al., 2019; Ringwaldt et al., 2023). Studies utilizing *S. scabiei* mites associated with canids and humans have shown the ability of mites to detect and travel toward nearby hosts and to gravitate toward sources of heat and light (Arlian et al., 1984; Arlian & Morgan, 2017), suggesting potential for off-host transmission. Laboratory studies of other mite variants have shown optimal survival in lower to moderate temperatures and quicker onset of mite mortality at hotter and freezing temperatures (Arlian, 1989; Arlian & Estes, 1984; Mellanby et al., 1942). It is thus possible that short-term environmental survival may be an important factor for transmission.

These results were later echoed for black bear *S. scabiei* mites: when incubated at different temperatures, the longest survival time was 13 days and occurred at cooler temperatures (4 °C) (Niedringhaus et al., 2019c). Further, previous lab-controlled studies of canid-associated *S. scabiei* survival and penetration ability showed that the duration of mites' ability to burrow and infest new skin after being held off the host is very shorter (no more than 36 hours in some cases at room temperature) (Arlian & Estes, 1984). This suggests that days-long environmental survival under specific weather conditions is likely possible, but long-term environmental survival is unlikely with even lower risk for actual mite infestation (Arlian & Estes, 1984; Niedringhaus et al., 2019c). However, these studies were conducted via controlled laboratory experiments and may not accurately reflect true environmental and habitat conditions. Additionally, the bear mite study utilized tissue and scrape material from freshly dead bears immediately following euthanasia (Niedringhaus et al., 2019c). How long these mites survive and remain on the bear host postmortem is unknown, thereby impacting the success of biological sample collection as well as our understanding of indirect transmission dynamics.

### *History and Epidemiology*

While *S. scabiei* is a new problem for black bear populations, it possesses a uniquely rich history as one of the oldest pathogens on record. *Sarcoptes scabiei* was first described in human hosts; writings of infestations in both humans and livestock go back to the Bible itself through references in Leviticus (Roncalli, 1987). *S. scabiei* became the first etiologic agent identified for a disease in 1687 when mites were finally discovered as the culprit behind scabietic lesions (Arlian & Morgan, 2017; Currier et al., 2011; Roncalli, 1987). Adding to its distinction, *S.*

*scabiei* is somewhat of an epidemiological anomaly: although many diseases of human concern are thought to originate in wild animal populations, it is hypothesized that *S. scabiei* spilled over into animal populations from human origin, and variations developed leading to different strains via continuous interbreeding on new animal hosts (Browne et al., 2022; Currier et al., 2011; Fain, 1978). Since its initial discovery, *S. scabiei* has been noted in the literature for centuries, and detailed descriptions exist (Arlian, 1989; Currier et al., 2011; Niedringhaus et al., 2019a). While it is considered somewhat less of a disease issue for humans in modern society, scabies is still considered a neglected tropical disease with hundreds to thousands of cases reported annually in some regions, and there have been sporadic epidemic events in the U.S. and other countries (Fain, 1978; Yabsley et al., 2025).

In the early 20th century, particular wildlife management strategies are likely to have cemented the mite's introduction into North American wildlife populations. In 1909, *S. scabiei* was intentionally introduced to canids to reduce populations. The Montana state veterinarian led a campaign to inoculate about 200 wolves and coyotes (*Canis latrans*) with *S. scabiei*, which quickly led to hundreds of reports of moribund and dead wolves and coyotes on the landscape (Knowles, 1909). After this inoculation event, coyotes with clinical signs of mange were reported in Wyoming, suggesting the potential spatial spread of sarcoptic mange following the initial introduction in Montana (Knowles, 1909). Over 100 years later, sarcoptic mange is an endemic parasite in many canid populations across the country; though not definitively proven, it is assumed that the widespread presence of sarcoptic mange on the landscape may have stemmed in part from this inoculation event.

Despite its rich history, it is still unclear what the evolutionary history of this assumed *S. scabiei* spillover has entailed. Some morphologic and physiological differences between mites from different hosts have been noted, suggesting host specificity and adaptation (Arlian, 1989). However, ample morphologic and genetic evidence to justify the delineation of true variants is lacking (Niedringhaus et al., 2019a). Research seeking to characterize the phylogenetic origins of *S. scabiei* in eastern U.S. bear populations ultimately found that sequences originated from numerous geographically distinct clades (Peltier et al., 2017). This work suggests that a single highly pathogenic strain of *S. scabiei* is not the cause of the increased emergence of sarcoptic bear mange (Peltier et al., 2017), but additional validation of these results and similar research among other populations is needed.

## SARCOPTIC MANGE IN WILDLIFE

### *Clinical Impacts and Pathology*

As stated, the typical lesions caused by *S. scabiei* infestation in the host are dermatitis and abnormalities of the epidermal skin layer, which appear several days to weeks after initial infestation (Stone et al., 1972; Fernando et al., 2024; Little et al., 1998). Induced by the burrowing behavior of the mites and their feeding on host cellular material, common clinical signs across most host species are crusting and scaling of the skin, alopecia, pruritus, seborrhea, hyperemia, erythema and hyperkeratosis (Van Neste, 1986; Arlian et al., 1988; Pence & Ueckermann, 2002; Arlian, 1989; Arlian & Morgan, 2017; Currier et al., 2011; Bornstein et al., 2001; Bornstein et al., 1995). Though these terms are mostly used to describe the disease in humans, infestations are classified as either crusted (Norwegian) or classical scabies, with the former involving higher mite burdens, more severely thickened crusts and keratotic plaques (Burks, 1956; Marcondes, 2017; Niedringhaus et al., 2019a).

Mites predominantly burrow through the stratum corneum layer of the skin, but can also reach the stratum granulosum and stratum spinosum (Morrison et al., 1982; Bornstein et al., 2001). Various proteinaceous excretions from the mite facilitate the digestion of host skin as tunnels are created (Arlian et al., 1988). Clinical manifestations are induced by this burrowing activity and the various irritants deposited by the mites, such as mite secretions, waste products, molted skins, eggshells, dead mites, etc. (Pence & Ueckermann, 2002; Yabsley et al., 2025). These products act as antigenic material, which induces an inflammatory hypersensitivity response in the host (Mellanby, 1944; Pence & Ueckermann, 2002). The resultant pruritic and dermatologic signs are a direct result of this hypersensitivity reaction (Fain, 1968).

Oftentimes, mite-induced disturbance to the skin layer also leads to secondary bacterial and fungal infections and self-mutilation by the host, further exacerbating disease. Bacteria present on the skin surface and inside the mites themselves gain entry to the host through mite tunnels (Fernando et al., 2024). Additionally, *S. scabiei* mites are thought to excrete immunomodulatory proteins that aid in digestion of host skin tissue, facilitating burrowing and feeding while simultaneously compromising host immune responses (Fernando et al., 2024; Mahmood et al., 2013). Proteins including aspartic, cysteine, and serine proteases have been detected in *S. scabiei* and play roles in blood and tissue digestion, invasion, virulence, mite hatching and molting, enzyme activation, immune evasion and host immunosuppression (Fernando et al., 2018, 2024; Fernando & Fischer, 2020; Holt et al., 2013). As a result, prolonged infestations and secondary complications lead to physical deterioration, dehydration, emaciation and eventual death (Arlian, 1989; Pence et al., 1983).

For different individuals and species, however, clinical signs can become more nuanced. Specifically, the nature and degree of the host's hypersensitivity response influences the course of disease (Pence & Ueckermann, 2002). Type I (immediate) hypersensitivity responses are characterized by proliferation and hyperplasia of mast cells and eosinophils, and are prevalent among severely affected species such as red foxes (*Vulpes vulpes*) (Little et al., 1998; Niedringhaus et al., 2019a). Conversely, Type IV (delayed) hypersensitivity response, characterized by accumulation of dermal T-lymphocytes, have been reported in humans and other domestic animals (Niedringhaus et al., 2019a; Tiffin et al., 2025; Zimmerman, 2012). The pathology of infestations in black bear and other wildlife, however, are less studied. Additionally, altered behavior and movement reductions are often observed as a product of the direct physiological changes induced by sarcoptic mange (Carricondo-Sanchez et al., 2017; Cypher et al., 2023; M. H. Murray et al., 2021; Süld et al., 2017). These decreases in movement patterns are likely in part due to the increased energy demands in alopecic individuals. Use of thermal cameras to monitor *S. scabiei*-infested wolves has shown significant heat loss, resulting in movement declines (Cross et al., 2016). The clinical signs and impacts of sarcoptic mange are thus far-reaching and often extend well past skin abnormalities.

While various acaricides exist for the treatment of sarcoptic mange, their efficacy and practicality in free-ranging populations is questionable. A 2019 review reported that treatment of sarcoptic mange in 30 species of captive and free-ranging wild mammals across 14 families had been documented in the literature, with the most commonly used drug being ivermectin (Rowe et al., 2019). Most of these studies were conducted on captive wildlife, with only a few in free-ranging populations and one where treatment was simultaneously administered to sympatric domestic animals and wildlife (Gakuya et al., 2012; Rowe et al., 2019). Success of treatment protocols in the available studies is variable and dependent on factors such as host species, drugs used, number of animals treated, and environmental settings (Martin et al., 2019; Rowe et al., 2019). The evaluation of successful treatment is also extremely limited by lack of long-term post-treatment monitoring, especially in wild animals or those released from captivity after treatment (Rowe et al., 2019). The lack of consensus on drug dosages, even among members of the same species, is an additional challenge to implementing treatment protocols (Kalema-Zikusoka et al., 2002; Rowe et al., 2019). While black bear mange has been treated with acaricides such as ivermectin or fluralaner in captive settings (Gillespie et al., 1984; Broadhurst et al., 2025; Wick & Hashem, 2019), long-term effectiveness in wild populations is understudied, with early evidence pointing toward poor improvement outcomes (Tiffin et al., 2024).

### *Prevalence and Distribution*

Sarcoptic mange is a globally pervasive parasite with an impressive record of hosts across numerous taxonomic orders. Affecting roughly 150 mammalian domestic and wild species across six continents, it is one of the broadest-spanning parasites both in terms of geographic and host range (Figures 1.3; 1.4), (Browne et al., 2022; Escobar et al., 2022; Niedringhaus et al., 2019a; Yabsley et al., 2025). After the identification of *S. scabiei* in domestic sheep, dubbed ‘sheep scab’, which was the first recorded animal host in 1809 (Currier et al., 2011), discoveries in new hosts steadily increased in both domestic and free-ranging wildlife species. Among wildlife hosts, Artiodactyl ungulates dominate the known susceptible hosts with 6 families and 53 known species, followed by Carnivora (8 families, 49 species); Rodentia (8 families, 13 species); Primates (4 families, 10 species); Diprotodontia (4 families, 6 species); Lagomorpha (1 family, 4 species); Erinaceidae (1 family, 4 species); Perissodactyla (2 families, 3 species); Pilosa (2 families, 2 species); Hyracoidea (1 family, 2 species); Pholidota (1 family, 1 species); and Peramelemorphia (1 family, 1 species) (Figure 1.4), (Escobar et al., 2022). As *S. scabiei* continues to garner increased attention and exploration, it is plausible that this already expansive host and geographic distribution will expand (Escobar et al., 2022).

Interestingly, geographic location appears to influence the primary species affected. For example, ungulates including chamois and ibex frequently experience sarcoptic mange outbreaks in Europe, while marsupials such as the wombat or koala face higher levels of mange in Australia (Escobar et al., 2022). In North America, canids including the red fox, coyote, and gray wolf (*Canis lupus*) are disproportionately affected; *S. scabiei* is also newly endemic in black bears on the continent (Escobar et al., 2022; Niedringhaus et al., 2019a). Host distribution and impacts for species in North America, including the black bear, will be further described.

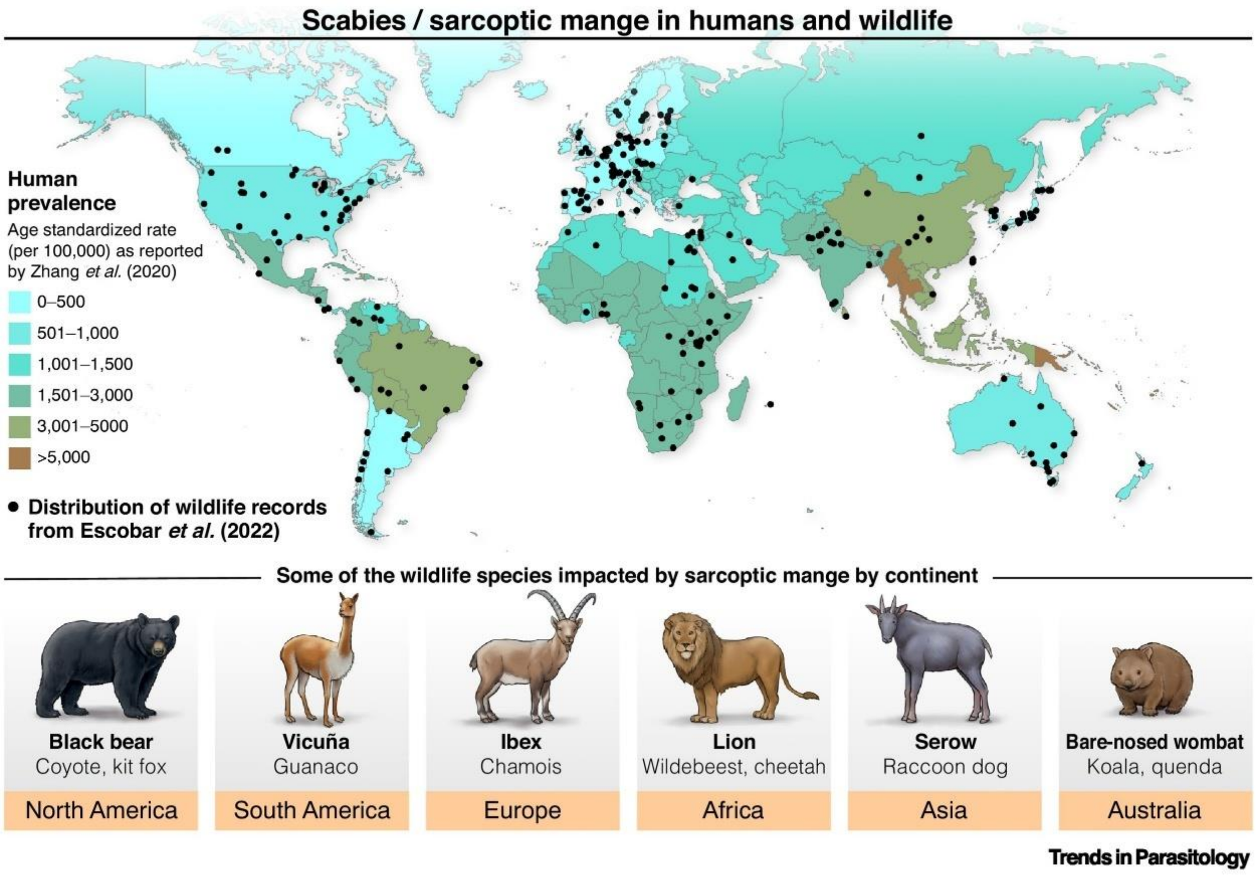


Figure 1.3. Global distribution of sarcoptic mange, showing human prevalence rates, locations of known wildlife outbreaks, and examples of common species affected in each region. (From Yabsley et al., 2025).

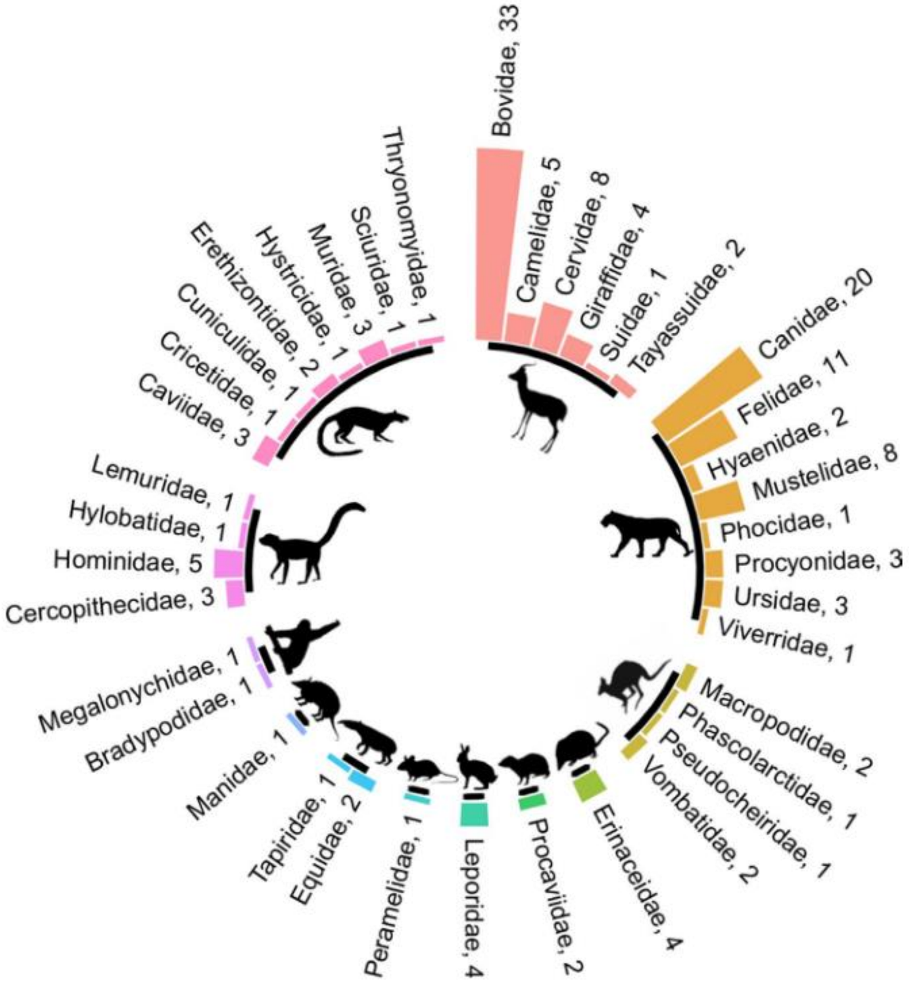


Figure 1.4. Wildlife taxa with reports of sarcoptic mange. Animal orders are shown by the black ring; families are represented by color groupings. Numbers represent the number of affected host species within each family. (From Escobar et al., 2022).

### *Host distribution in North America*

Historically, the most reported sarcoptic mange outbreaks have been in canid species (Astorga et al., 2018; Niedringhaus et al., 2019a). The reasons behind this apparent increased proclivity to develop disease and suffer impacts at the population level are not understood entirely, but is likely due in part to their inclination to mount dramatic immediate hypersensitivity responses as well as the aforementioned initial purposeful introduction of this parasite into wild wolf and coyote populations (Little et al., 1998; Knowles, 1909). Since that introduction event, *S. scabiei* has been able to maintain endemicity in these populations for several decades. Sarcoptic mange has been extensively studied in gray wolves, an already imperiled North American species, in Yellowstone National Park (Almberg et al., 2012; DeCandia et al., 2021; Smith & Almberg, 2007). Other North American canids known to be affected by sarcoptic mange are summarized in a literature review by Niedringhaus et al. (2019a) and include red foxes, gray foxes (*Urocyon cinereoargenteus*), kit foxes (*Vulpes macrotis mutica*), coyotes, red wolves (*Canis rufus*) and Mexican wolves (*Canis lupus baileyi*). Less common North American hosts include the raccoon (*Procyon lotor*), North American porcupine (*Erethizon dorsatum*), white-tailed deer (*Odocoileus virginianus*), bighorn sheep (*Ovis canadensis*), fox squirrel (*Sciurus niger*), swamp rabbit (*Sylvilagus aquaticus*), house mouse (*Mus musculus*), fisher (*Martes pennanti*) and feral swine (*Sus scrofa*). The American black bear, though once on this list of uncommon hosts, has surpassed these species in disease prevalence to become another hallmark host for mange in North America. Systematic sampling and observation has not been conducted across the continent, however, leaving the true prevalence and effects of mange in North American wildlife incompletely understood (Astorga et al., 2018).

## SARCOPTIC MANGE IN BLACK BEARS

### *Black Bear Health and Ecology*

The American black bear is a solitary, omnivorous game species of great ecological and cultural significance. Although the black bear has historically experienced large population declines in several parts of its North American range due to habitat loss and overexploitation, it now represents a modern success story due to management and conservation intervention

(Miller, 1990; Scheick & McCown, 2014). Since the 1980s, the eastern black bear range has been expanding, with populations distributed across most U.S. states throughout over 10 million square kilometers (Scheick & McCown, 2014). Nevertheless, this species is not immune to challenges, including habitat fragmentation and destruction, conflict with humans, and health impacts (Bard & Cain, 2019; Dixon et al., 2007; Spencer et al., 2007). As their populations rebound and available habitat becomes increasingly limited, population health becomes especially important in terms of disease transmission dynamics.

Although disease is not typically considered to be a significant threat to black bear populations, black bears are susceptible to many bacterial, viral and parasitic pathogens. Aside from mange, other diseases in North American black bears include tick borne diseases, canine distemper virus, canine parvovirus, adenovirus, plague (*Yersinia pestis*), Tularemia, west nile virus, *Toxoplasma gondii*, brucellosis, *Sarcocystis, Baylisascaris, Babesia, Trichinella*, and various other ecto- and endoparasites. However, not all diseases listed are always clinically detrimental to individuals or impactful to overall bear population health (Collins et al., 1984; Bard & Cain, 2019; Binninger et al., 1980; Cottrell et al., 2013; Lee et al., 2021; Riese, 2023).

### *Sarcoptic Mange Emergence in Black Bears*

Sarcoptic mange reports in black bears date back to 1987, when North America's first documented case was reported in Michigan (Schmitt et al., 1987). A few subsequent cases were reported (Schmitt et al., 1987), but the sustained presence in the state's black bear population has still not been documented. Unfortunately, this was not the case for nearby states a few years later: the first bear with sarcoptic mange in Pennsylvania was observed in 1991 and was followed by hundreds of cases over the next several years (Niedringhaus et al., 2019d). Enzootic mange cases also were reported soon after in New York, Virginia, and West Virginia

(Niedringhaus et al., 2019d). Currently, Maryland, Georgia, Arkansas, Oklahoma, and Missouri also have reported cases, but disease is not considered endemic and mange is still emerging in these locations. With this pattern of continued spread, state wildlife agencies across the eastern U.S. are attempting to grapple with this new threat. There has been a growing amount of active research in the wake of these increased black bear mange cases, but a full picture of the mechanisms driving this surge in geographic range and prevalence remains incomplete, along with the potential population-level impacts (Niedringhaus et al., 2019d; Peltier et al., 2017).

## SURVEILLANCE TACTICS

### *Diagnostic Techniques*

Initial detection of sarcoptic mange is typically accomplished with syndromic surveillance (Tiffin et al., 2020), but for accurate diagnosis, individual host sampling and identification of the mite species is required. This is critical because there are multiple mites that can cause mange lesions in bears, and there are also non-mite causes of skin lesions (endocrine, bacterial/fungal, etc.). Several diagnostic approaches have been implemented with variable success, including histology, serology, molecular analysis, and microscopic examination of skin scrapes (Escobar et al., 2022; Niedringhaus et al., 2019a; Peltier et al., 2018; Tiffin et al., 2020). Validation of these approaches on a broader scale is still in its infancy.

Collecting skin scrapes and morphologically identifying mites under a microscope is currently the most utilized method and is considered the best practice for species confirmation (Escobar et al., 2022; Niedringhaus et al., 2019a). However, disease manifestation and relative host mite burdens are variable across different species and individual animals (Niedringhaus et al., 2019a). Severe clinical disease can be observed with low mite burden, and high mite burdens can also be present on animals with less dramatic clinical manifestation (Arlian & Morgan, 2017; Tiffin et al., 2020). In canids, for example, severe lesions and disease are often observed despite low mite burdens being present (Niedringhaus et al., 2019a). Thus, the variability in mite density and clinical presentation complicates the accurate identification, sampling, and diagnosis of cases.

Conversely, even if skin scrapings are positive for mites, this approach does not provide accurate mite burden estimates. Considering the variation in clinical lesions, scrapes are not uniformly collected (Tiffin et al., 2020). Mites remaining burrowed deeper in the epidermis during sample collection may also be missed, leading to potential underrepresentation of actual mite burden in a superficial skin scrape (Arlian & Morgan, 2017; Tiffin et al., 2020). To more accurately quantify mite burdens, recent work has sought to develop standardized protocols involving the digestion of tissue samples and subsequent enumeration of mites (Tiffin et al., 2020). Future research directions should include further validation of this methodology across different species, including evaluating mite density and observable disease symptoms in the bear host. Additionally, while anecdotal evidence suggests that particular body regions of the bear host, including the head, rump, and flank, tend to harbor the most mites, this has not been quantified. Mite enumeration protocols may therefore have the potential to inform this question and to dictate best practice sampling techniques for the future.

### *Movement Analyses*

Tracking movement patterns, behavior and space use are other useful parameters to investigate in populations with sarcoptic mange. Several studies, particularly in canids, have shown spatial patterns in mange spread and host space use. Particularly, the impacts of anthropogenic alterations to habitat and increased human-wildlife contact have the potential to impact *S. scabiei* transmission. For example, reduced home range sizes and/or differential use of anthropogenic resources and human settlements have been noted in foxes, coyotes and raccoon dogs with mange (Carricondo-Sanchez et al., 2017; Murray et al., 2021; Süld et al., 2017). Other changes to behavior, such as shifting diel activity and foraging patterns, have also been noted in canids and wombats (Cross et al., 2016; Simpson et al., 2016). In addition to aiding population monitoring, movement studies can help to better understand sarcoptic mange transmission dynamics: models have provided evidence for density-dependent relationships in some populations (Almberg et al., 2012; Gortázar et al., 1998; Uraguchi et al., 2014) and frequency-dependent relationships in others (Carricondo-Sanchez et al., 2017; Devenish-Nelson et al., 2014), with discordant results even among different populations of the same species. The available studies therefore signal that sarcoptic mange spread is complex and likely dependent on the particular intricacies of the species, ecosystem, and population at hand.

Spatial studies on bears with sarcoptic mange, on the other hand, are much more limited. A 2014 thesis studying Pennsylvania's black bear population explored whether areas with greater impervious land cover harbored more bear mange (Sommerer, 2014). The author predicted that bears in areas with more impervious land cover were occupying more highly urbanized areas. Additionally, it was assumed that bears in areas with more impervious land cover were in increased contact, thus insinuating a density-dependent disease relationship. It was ultimately found that there was no significant relationship between impervious land cover and the occurrence of mange in black bears. The highest concentration of mange observations were actually found in an area dominated by rural and forested land, pointing instead toward a potential relationship between bear mange and less anthropogenic areas (Sommerer, 2014). While this may truly reflect the absence of a density-dependent relationship and no association between mange and urban areas, it is also possible that the impervious land cover variable alone may not have properly characterized areas with growing urbanization, and/or that the assumption of higher bear densities in urban areas was false. Additionally, even if the conclusions were accurate, the aforementioned conflicting studies in foxes and other canids show that what may be true for one state's bear population may not be true for all bear populations with mange. Another recent thesis found trends in diseased bear movement, with collared mange bears moving less than other healthy individuals in Pennsylvania (Tiffin, 2022). Bears with severe mite burdens in particular had significantly lower mean step lengths (Tiffin, 2022), calling into question the influence of disease severity on spatial patterns.

In general, the spatial epidemiology of *S. scabiei* is still unclear. The true extent of North American sarcoptic mange distribution, transmission pathways, biogeographical disease patterns, environmental factors and their interactions with different hosts require further exploration (Astorga et al., 2018). It is therefore helpful to consider sarcoptic mange in a spatial context to more fully understand this disease issue.

## RESOURCE-SELECTION FUNCTION MODELS AS A TOOL FOR WILDLIFE STUDIES

Although various models exist in modern ecological science to examine animal space use, resource-selection function (RSF) models are one commonly used approach. RSF models are used to analyze how an individual animal or population utilizes space through estimation of their apparent selection of a particular environmental resource. Rooted in basic principles of natural selection, a resource-selection function calculates values which are proportional to the probability of use of a resource (Boyce et al., 2002). This framework accounts for how much of a resource is used by an animal, or the proportion with which the animal chooses to interact with a particular resource, and the availability of the resource, or how much of a resource is present in an area that the animal could interact with and select for. In essence, these models allow managers to assess what environmental characteristics may be important for a population by evaluating the probability of an animal using a certain spatial location relative to the availability of some resource or habitat characteristic in that location.  As a result, they have the ability to elucidate where areas of critical habitat may be, which can inform where to concentrate management efforts, how land use changes may impact a population, and more.

After delineation of a study area, data are analyzed based on observations of animal occurrence, typically referred to as “used” points, compared with “unused” or “available” points where an observation could have been made. These available locations can be derived from either random or systematic sampling of the study area. Several models may be employed to examine these relationships, but the most common is a logistic regression binomial generalized linear model (GLM) (Boyce et al., 2002). RSFs can be analyzed at finer scales, which are useful to examine questions such as foraging preferences, and larger scales, which can inform questions related to individual or population home range preferences. Consideration of scale when building an RSF is paramount, as ecological interactions occur at differing spatial scales (Boyce, 2006; DeCesare et al., 2012), and the scale chosen is liable to alter outcomes.

For example, one common use of RSF models is predicting the likelihood of interspecies interactions. In the case of human conflict-prone megafauna, this may include characterization of interactions with humans. Merkle et al. (2011) employed RSF modeling to identify areas with high potential for human-black bear interactions in Missoula, MT. They were able to determine that the probability of observing a human-black bear interaction within the study area was influenced by distance to forests and water bodies, and the housing density in an area. This allowed them to generate a heat map showing areas most likely to experience human-black bear interactions (Merkle et al., 2011).

RSFs are less commonly used in the context of wildlife disease monitoring, but represent an interesting and novel way to explore epidemiological questions as spatial disease transmission dynamics gain increased attention. Dinh et al. (2021) used RSF models to compare resource selection between wild and ranched white-tailed deer (*Odocoileus virginianus*) in areas with epizootic hemorrhagic disease (EHD) outbreaks to help explain the higher disease prevalence in ranched deer. This work showed that the ranched deer were more likely to select for habitats more conducive to EHD-relevant vector species, offering a potential explanation for the increased disease risk within the ranched population. Modeling efforts also led to identification of areas with higher risk for disease transmission based on deer selection preferences (Dinh et al., 2021). Another study evaluated elk resource selection in tandem with identification of areas with *Bacillus anthracis*, the causative agent of anthrax, to evaluate the probability of spatial overlap occurring between elk and *B. anthracis* presence (Morris et al., 2016). Areas of high overlap were observed, and risk areas that could serve as priority locations for disease surveillance and management were identified (Morris et al., 2016). These studies serve as examples of how resource-selection analyses can be used to understand host-pathogen disease ecology and potentially identify at-risk populations and locations.

With the potential for sarcoptic mange to influence bear movement in a variety of ways, (i.e., reduced motility, diminished foraging ability, forays into unusual areas) RSFs may be useful to characterize diseased animal activity and altered behavioral patterns. These models could help inform how diseased bears are using the landscape and whether or not they are selecting for resources differently than their healthy counterparts. Additionally, RSFs may elucidate areas with higher risk for sarcoptic mange transmission and/or increased contact between people and diseased animals. This information could not only enlighten our understanding of the pathophysiological impacts of sarcoptic mange in bears, but also inform where wildlife personnel can target mange mitigation, management, and public education efforts. In this work, the probability of reporting a case of bear mange is evaluated based on the level of urbanization and anthropogenic disturbance in a location, investigating whether the same patterns described in other species with mange exist in black bears. The use of public reporting data for diseased animals in an RSF context is explored, representing a novel way to tailor disease reporting data.

## MANAGEMENT IMPLICATIONS

As an emerging, dynamic disease challenge in North American black bears, the true threat of sarcoptic mange for bear population viability is still largely unknown. While individual morbidity, mortality, and severe disease effects are well-documented, larger-scale impacts on populations are still extremely unclear in this evolving situation. What is more, stories of individual survival and recovery are also shrouded within the casualties, although often masked by the inherent reporting bias towards severely ill and moribund individuals; this adds further complexity to predictions regarding long-term population impacts. However, in combination with habitat losses and other pressures, mange has the potential to augment population declines. Thus, baseline investigations to better characterize the epidemiology of this disease in a new host are critical, especially in a valued game species. The importance of addressing these questions is further weighted by the zoonotic potential of *S. scabiei*. In a world with an ever-growing human population and ever-shrinking habitat space for other animals, sarcoptic mange is a prime example of a ‘One Health’ pathogen of critical importance. To safeguard human, bear, and ecosystem health, it is necessary to deepen our understanding of sarcoptic mange; this work attempts to primarily address the bear health piece of this puzzle and continue laying the fundamental groundwork to understand how sarcoptic mange impacts bears on the landscape.

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# CHAPTER II

# EVALUATION OF *SARCOPTES SCABIEI* MITE BURDENS ON AMERICAN BLACK BEARS (*URSUS AMERICANUS*) WITH SARCOPTIC MANGE [1]

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[1] Broadhurst, J.R., Francisco, R., Rivera Reyes, J., Berdecia-Martinez, V., Tugend, C., Martin, K., Carpenter, C., Barton, E., Bloodgood, J.C., McNamee, T., Haynes, E., Michel T. Kohl, M.T., and Yabsley, M.J. To be submitted to a peer-reviewed journal.

## Abstract

Sarcoptic mange caused by the *Sarcoptes scabiei* mite is a zoonotic skin disease with an extensive host and geographic distribution. Despite a long-standing presence on the landscape, *S. scabiei* has emerged in American black bear (*Ursus americanus*) populations in the eastern U.S. only within the last few decades. The reasons for this recent emergence and the host-pathogen dynamics of this new system are largely unknown. The present study sought to characterize levels of mite infestation on the bear host, a fundamental yet underexplored step to understanding disease pathogenesis and improving surveillance techniques. Skin samples were collected from sarcoptic mange bears and apparently healthy controls from populations with endemic mange presence from three states (NY, VA, WV). Samples were taken from five predetermined body regions on the bear with the additional goal of determining whether mite burdens varied on different areas of the body. Animals were quantitatively scored to determine grade of clinical severity (i.e., amount of hair loss, body condition, skin condition) and samples were chemically digested to elucidate mites for counting. Remarkably high mite burdens were discovered (≤ 5,299 in a single biopsy), but burdens were not correlated with the level of clinical disease severity. Mite burdens were also not homogenous throughout all sampled body regions, with the forearm, rump and flank having the largest number of mites and highest relatedness. These findings help inform disease progression in black bears, disease monitoring and surveillance, and best practices for field sample collections.

## Introduction

Mange is a skin condition of animals caused by parasitic mite infestations. Sarcoptic mange caused by *Sarcoptes scabiei* is one of the most important forms of mange in mammals due to its extensive host and geographic distribution, population-level impacts across numerous domestic and wild species, and zoonotic potential (Fain, 1991; Escobar et al., 2022; Bornstein et al., 2001). This mite also causes scabies in humans, predominately in tropical regions of the world (Yabsley et al., 2025). Clinical manifestations include intense pruritus, alopecia, hyperkeratosis, dermal crusting and erythema; clinical signs are caused by the mites' creation of tunnels in the epidermal layer of the host skin where mites survive and reproduce (Pence & Ueckermann, 2002; Niedringhaus et al., 2019a; Walter & Proctor, 2013). While disease can be self-limiting in some cases, epizootics involving mortalities and population-level impacts due to secondary complications have been reported in several species (Niedringhaus et al., 2019a; Bornstein et al., 2001). In these instances, hypersensitivity responses from mite infestation lead to secondary infections, emaciation, dehydration, and eventual death (Arlian et al., 1988; Niedringhaus et al., 2019a).

In North America, canids including coyotes (*Canis latrans*), gray wolves (*Canis lupus*) and red foxes (*Vulpes vulpes*) have historically had the highest disease prevalence (Astorga et al., 2018; Niedringhaus et al., 2019a). The American black bear (*Ursus americanus*) was not historically affected by sarcoptic mange in North America, but the disease has emerged in bear populations in the eastern U.S. within the last few decades (Niedringhaus et al., 2019b). A growing number of states have reported notable numbers of mange-related bear morbidities and mortalities, raising concerns for future bear population health (Niedringhaus et al., 2019b). Several hypotheses have been proposed to explain why specific bear populations may be predisposed to these outbreaks, including geographic spread of the parasite, presence of co-infections, and increased inter- and intra- species congregations (Niedringhaus et al., 2019b), but the driving forces behind the emergence of this parasite in a new host species are not well understood. However, the rapid expansion of *S. scabiei* in black bear populations and its potential to impact bear health on a large scale necessitates investigation into the epidemiology and pathology of this disease system.

Syndromic surveillance is often used to initially detect sarcoptic mange cases (Tiffin et al., 2020), but mite identification is still required for diagnosis as there multiple mite species that can cause mange in bears (Broadhurst et al., 2025; Desch, 1995; Klompen, 1993; Niedringhaus et al., 2019a; Niedringhaus et al., 2021). Several methods have been employed to diagnose cases, but cytology of skin scrape material is considered best practice to reliably confirm and morphologically identify *S. scabiei* (Escobar et al., 2022; Niedringhaus et al., 2019a; Peltier et al., 2018). However, the accuracy of this diagnostic tool is hampered by differing disease manifestations and host hypersensitivity responses among different species and individual animals (Davis & Moon, 1990; Little et al., 1998; Niedringhaus et al., 2019a). Severe clinical presentation of disease can be observed with a low number of mites recovered on skin scrapes, and relatively high mite burdens can also be found on animals with less severe clinical manifestation (Alasaad et al., 2008; Arlian & Morgan, 2017; Tiffin et al., 2020). For example, canids tend to have lower mite burdens but often still present with severe disease, challenging definitive diagnoses; conversely, larger numbers of mites are often found on other species (Arlian et al., 1988; Niedringhaus et al., 2019a; Bornstein et al., 2001). Variability in mite density and clinical presentation therefore can impede accurate identification, sampling and diagnosis of cases. Anecdotally, it is often easier to find *S. scabiei* mites in bear skin scrapes to confirm diagnoses compared to in canid samples, even in dramatically clinically impacted individuals; however, this has not been verified. Additionally, superficial skin scrapes are likely to miss the majority of mites burrowed deeper in the skin, further complicating our ability to ascertain true mite burdens. Thus, research efforts to better understand *S. scabiei* infestation in wildlife are currently hindered by lack of accurate methods to quantify mite burdens.

Previous research has employed skin sample digestion to visualize and quantify mites from infested host skin in other species, providing some preliminary information on mite burdens (Arlian, 1989; Carvalho et al., 2016; Davis & Moon, 1990; Little et al., 1998; Mumcuoglu, 1990; Trainer & Hale, 1969; Zimmerman, 2012). Recently, Tiffin et al. (2020) piloted an updated skin digestion protocol to facilitate quantification of mite burdens in animals with sarcoptic mange. This work resulted in successful estimation of *S. scabiei* mite counts in samples from seven individuals from Pennsylvania, including two black bears (Tiffin et al., 2020).

To better investigate mite burdens and characterize sarcoptic mange infestation in eastern U.S. black bears, we validated and adapted this protocol on a larger number of bears sourced from multiple populations with endemic presence of *S. scabiei* across several states. Namely, we intended to explore the potential correlation between mite burden and disease severity, which has not been formally evaluated in black bears. As numerous state agencies attempt to grapple with this new challenge to their black bear populations, sarcoptic mange is currently surveilled in a variety of ways; there is little congruity in sample collection procedures and scant available guidance on diagnostic methodology for assessing mange in black bear populations. This produces a litany of complications for the effective identification and management of black bear mange cases. This study therefore also explored whether different mite burdens could be found on skin samples from various regions of the host body. This information has the potential to inform best practices for mange surveillance through identification of areas with high mite burdens to obtain the best representative diagnostic samples. It is hoped that this work will help establish standardized sample collection procedures that can be shared among field biologists to streamline collection techniques, better understand *S. scabiei* pathology in the black bear, and improve sarcoptic mange surveillance.

## Methods

### *Sample Collection*

Samples were accepted from three states: New York (NY), Virginia (VA), and West Virginia (WV), which all reported their first sarcoptic mange cases around the same time period (early to mid-2000s) and have since then observed endemic levels of mange in bear populations. Black bears included in the study were either humanely euthanized due to severe mange by state agency personnel or were found freshly dead

From April 2023 to December 2024, 38 bears were submitted for inclusion in the study, including 27 animals with confirmed sarcoptic mange and 11 negative control bears without clinical signs of mange. Control bears originated from the same populations with endemic mange presence but did not have overt lesions and skin scrapes were negative for mites. Mange-positive bears were subdivided into one of three categories of sarcoptic mange severity (mild, moderate, or severe) as determined by a mange severity scaling system that combined qualitative and quantitative evaluations of clinical signs and lesions. Qualitative methods included the biologists’ assessment of mange severity at the time of sample collection given a descriptor for each severity classification (Table 2.1). Quantitative methods included the completion of a modified ‘mange matrix’ form adapted from Tiffin et al. (2024, 2025). The matrix included three categories ranking levels of alopecia, skin condition and body condition. For each category, clinical appearance could be ranked from 0 (suggestive of a normal, non-clinically diseased animal) to 3 (suggestive of most severe clinical manifestation), with provided descriptions accompanying each rank (Table 2.2). Scores for each of the three categories were summed to yield a total mange severity score. Thus, mange severity scores could range from 0, suggesting no clinical signs of mange, to 9, suggesting the most severe clinical signs of mange (Table 2.2). Animals with total severity scores of 1-3 were considered mildly diseased; 4-6 moderate; and 7-9 severe.

Once the severity of mange was established, state agency personnel collected sections of skin that were at least 12x12 cm from five body regions on each individual bear: the ear (tip of the pinna down to base), cheek, forearm, flank, and rump (Figure 2.1). Collection sites were chosen based on anecdotal evidence of areas that tend to yield positive skin scrapes in individuals with mange. When possible, skin samples containing both unaffected skin and mange lesions were taken from each body region. Samples were stored at -20°C until processing.

Table 2.1. Disease severity classifications and associated descriptions of clinical signs for the qualitative assessment of American black bears (*Ursus americanus*) with *Sarcoptes scabiei* infestation.

| **Qualitative Severity Classification** | **Description** |
|---|---|
| Mild | Good weight, small areas of crusted skin, minimal to patchy hair loss |
| Moderate | Thin, patches of crusted +/- thickened skin, patchy hair loss |
| Severe | Emaciated, diffuse skin crusting & thickening, hair loss >1/2 of body |
| Recovering | Good weight, smooth dark skin, minimal to extensive hair loss |

Table 2.2. ‘Mange matrix’ used to quantitatively assess disease severity of American black bears (*Ursus americanus*) with *Sarcoptes scabiei* infestation. Categories include rankings for level of host hair loss, skin condition, and body condition. Numerical rankings from each severity category are then tallied to compute the total mange severity score used in analyses.

| **Category** | **0** | **1** | **2** | **3** | **Severity Category (0-3)** |
|---|---|---|---|---|---|
| **Hair Loss** | None | Hair missing from less than 1/3 of body | Hair missing from 1/3 to 2/3 of body | Hair missing from more than 2/3 of body | |
| **Skin Condition** | Normal | Skin not thickened or pigmented, areas of scaly skin small and diffuse | Patches of thickened, crusted, or black pigmented skin | Large areas of thickened, crusted skin, debris flaking from skin or on hair shafts; strong odor | |
| **Body Condition** | Normal | Below Average; vertebrae knobby, pelvic crest and ribs can be felt but not protruding | Poor; spinal vertebrae well defined, pelvic crest and ribs visible, skull structures felt but not visible | Emaciated; skeletal muscle gone, zygomatic arches visible, eyes sunken | |
| | | | | **Mange Severity Total Score (0-9)** | |

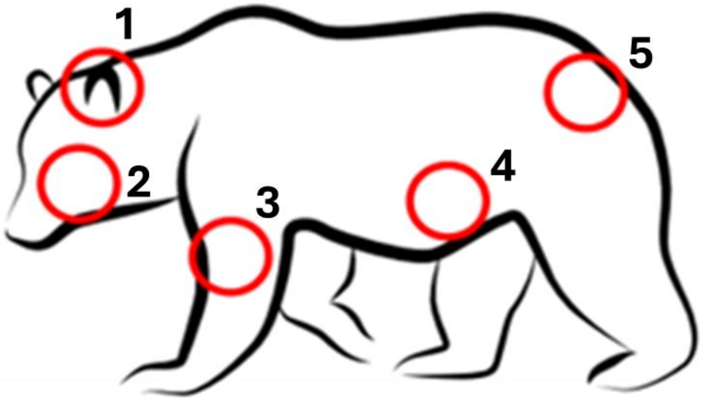

Figure 2.1. Skin sample collection sites on the American black bear (*Ursus americanus*) tested for *Sarcoptes scabiei* mite burdens. Circled body regions include the ear (1), cheek (2), forearm (3), flank (4) and rump (5).

### *Sample Processing*

A total of 190 skin samples were processed from 38 animals (5 sites/bear). All submitted pieces of skin were cut to a standardized size of 6x6 cm from which five 6mm biopsy punch (McKesson Argent, India) samples were taken. Punches were taken from each corner and center of the skin sample and were labeled 1-5. A notch was taken from the top left corner of each sample to keep track of biopsy punch locations and numbers.

Each biopsy punch was placed in a gridded petri-dish with approximately 60 mL of 10% KOH solution (KOH pellets, Fisher Chemical, Ottawa, ON, Canada) and incubated at 55°C for 12 hours (Tiffin et al., 2020). After 12 hours of digestion, the petri dish was removed from incubation and 50% citric acid solution (Aqua Solutions, Deer Park, TX) was added dropwise to the solution until a neutral pH was achieved (confirmed with paper pH strip indicators [Fisher Scientific, Waltham, MA]) This was done to prevent additional tissue digestion past the 12-hour period during the counting process. Petri dishes were examined under a dissecting scope (0.7 X to 3.0 X magnification). We recorded the total number of mites per plate as well as the total of each life stage: adult female (≥ 0.3 mm), adult male (0.2-0.29 mm), juvenile mites (larvae and nymphs), and eggs.

### *Statistical Analysis*

To explore the association between mite burden and clinical mange severity, the number of mites on each of the five biopsy punches per body region were summed to generate a total count for each body region. Total counts for each body region were also added to generate a grand total across all five regions. Correlations between total counts by body region were assessed prior to model fitting. The numerical mange severity score based on mite count was predicted using generalized linear mixed effect ordinal logistic regression models with a cumulative logit link. Body region totals and grand total counts were used to create a suite of univariate and additive models.

To evaluate potential differences in mite burdens on different host body areas, mite counts across all biopsy samples were analyzed. Generalized linear mixed effect negative binomial regression models with a log link function were fitted to predict mite count as a function of host body region. Predicted marginal means for each group were calculated and pairwise comparisons were performed with a Sidak adjustment. All models were ranked via AIC corrected for small sample sizes. Analyses were performed using Program R (version 4.4.3, R Core Team 2023).

## Results

Mite burdens were counted from 950 total biopsy punches (190 from 190 skin sections (5 skin sections per bear, n = 38 individual animals). Individuals included in the study were 11 control bears with no disease, 7 moderately diseased bears (severity score of 4-6), and 20 severely diseased bears (severity score of 7-9) (Table 2.3). Unfortunately, no bears classified as mild were submitted. Nearly all of the mites identified were *S. scabiei* based on morphologic characteristics, but some bears were co-infested and also had small numbers of *Ursicoptes americanus* mites. Total mite counts per one 6 mm biopsy punch sample on all diseased bears (n = 27) ranged from 0 to 5,299 mites (mean = 599.00; median = 385). Total mite counts per individual bear (summation of all 25 biopsy punches) ranged from 1,902 to 26,240 mites (mean = 13,975.07; median = 12,990.00). No mites were detected in the 11 control bears. Pearson correlation coefficients between total counts by body region were low (all $r < 0.4$).

Models including variations of mite counts on diseased bears (n = 27) showed that mite burdens were not a significant predictor of mange severity scores for moderately and severely diseased bears (Table 2.4). The model including the total mite burden on the forearm had a notable effect size (β = 0.62; 95% CI = -0.19, 1.77); however, it was not significant (p = 0.20), and the more parsimonious null model had slightly better AIC support (ΔAIC = 0.87), indicating weak evidence for the contribution of mite count to influence disease severity (Table 2.4).

Table 2.3. Number of American black bears (*Ursus americanus*) submitted to investigate *Sarcoptes scabiei* mite burdens by state of origin and clinical severity level. Bears categorized as normal reflect bears with a numerical severity score of 0; mild bears reflect severity scores of 1-3; moderate bears reflect severity scores of 4-6; severe bears reflect severity scores of 7-9.

| | **Normal** | **Mild** | **Moderate** | **Severe** | **Total** |
|---|---|---|---|---|---|
| **VA** | 1 | 0 | 5 | 3 | 9 |
| **WV** | 4 | 0 | 0 | 11 | 15 |
| **NY** | 6 | 0 | 2 | 6 | 14 |
| | | | | | **38** |

Table 2.4. Model weights for the generalized linear mixed effect ordinal logistic regression model candidates tested to predict clinical disease severity in American black bears (*Ursus americanus*) as a function of *Sarcoptes scabiei* counts. Candidates included a null model, univariate models, and an additive model.

| **Model** | **K** | **AICc** | **ΔAICc** | **AICc Wt** | **Cum. Wt** | **LL** |
|---|---|---|---|---|---|---|
| Null | 4 | 90.28 | 0.00 | 0.344 | 0.34 | -40.23 |
| Mange Severity ~ Forearm Total Mite Count | 5 | 91.16 | 0.87 | 0.222 | 0.57 | -39.15 |
| Mange Severity ~ Rump Total Mite Count | 5 | 92.63 | 2.34 | 0.107 | 0.67 | -39.88 |
| Mange Severity ~ Grand Total Mite Count | 5 | 93.01 | 2.73 | 0.088 | 0.76 | -40.08 |
| Mange Severity ~ Flank Total Mite Count | 5 | 93.17 | 2.89 | 0.081 | 0.84 | -40.16 |
| Mange Severity ~ Ear Total Mite Count | 5 | 93.18 | 2.90 | 0.081 | 0.92 | -40.16 |
| Mange Severity ~ Cheek Total Mite Count | 5 | 93.30 | 3.02 | 0.076 | 1.00 | -40.22 |
| Mange Severity ~ Rump + Ear + Flank + Cheek + Forearm Total Mite Counts | 9 | 102.63 | 12.34 | 0.001 | 1.00 | -37.02 |

A model including a covariate for host body region with individual bears as a random effect showed increased power over the null to predict mite burdens on biopsy punch samples from clinically diseased bears (n = 675) (Table 2.5). This was chosen as the final model used to compute marginal means pairwise comparisons (Table 2.6).

Table 2.5. Model weights for the generalized linear mixed effect negative binomial regression model candidates tested to predict *Sarcoptes scabiei* count as a function of American black bear (*Ursus americanus*) host body region sampled. Candidates included a null model and a model including a host body region covariate.

| **Model** | **K** | **AICc** | **ΔAICc** | **AICc Wt** | **Cum. Wt** | **LL** |
|---|---|---|---|---|---|---|
| Mite Count ~ Body Region + (1\|Bear ID) | 7 | 9651.13 | 0.00 | 1.00 | 1.00 | -4818.48 |
| Null | 2 | 9868.70 | 217.57 | 0.00 | 1.00 | -4932.34 |

Table 2.6. Parameter estimates for fixed effects in the final generalized linear mixed effect model to predict *Sarcoptes scabiei* burdens in American black bears (*Ursus americanus*) with sarcoptic mange as a function of host body region sampled. Coefficients reflect exponentiated values. 95% confidence intervals are shown.

| **Parameter** | **Coefficient** | **SE** | **Lower CI** | **Upper CI** | **z** | **p** |
|---|---|---|---|---|---|---|
| (Intercept) | 487.07 | 54.10 | 391.78 | 605.54 | 55.71 | 0.00 |
| Ear | 0.55 | 0.06 | 0.45 | 0.67 | -5.89 | 0.00 |
| Flank | 1.12 | 0.10 | 0.93 | 1.34 | 1.20 | 0.23 |
| Forearm | 1.39 | 0.12 | 1.17 | 1.64 | 3.76 | 0.00 |
| Rump | 1.17 | 0.11 | 0.98 | 1.40 | 1.78 | 0.07 |

Estimated marginal means for each body region group revealed estimated mite counts between 267 to 676 mites per individual 6 mm biopsy punch. The ear generally harbored the smallest number of mites, while the forearm had the greatest predicted mite burden (Table 2.7).

Table 2.7. Predicted marginal means derived from the final model for each body region sampled for *Sarcoptes scabiei* mite burdens on the American black bear (*Ursus americanus*) host. Coefficients reflect exponentiated values. 95% confidence intervals are shown.

| **Location** | **Response** | **SE** | **Lower CI** | **Upper CI** |
|---|---|---|---|---|
| Cheek | 487.07 | 54.10 | 391.78 | 605.54 |
| Ear | 266.81 | 32.49 | 210.16 | 338.72 |
| Flank | 544.51 | 59.77 | 439.11 | 675.20 |
| Forearm | 675.51 | 72.22 | 547.81 | 832.97 |
| Rump | 572.07 | 62.04 | 462.53 | 707.56 |

Pairwise comparisons using estimated marginal means with Sidak adjustment showed significantly lower mite burdens on the ear relative to all other body regions (Table 2.8; Figure 2.2). Significantly lower mite burdens were also seen on the cheek compared to the forearm (IRR = 0.72; p = 0.00). Other pairwise comparisons were not statistically significant (Table 2.8; Figure 2.2).

Table 2.8. Estimated differences in *Sarcoptes scabiei* burdens on different body regions of the American black bear (*Ursus americanus*) using Sidak-adjusted pairwise comparisons between predicted marginal means for each body region derived from the final model.

| **Contrast** | **Ratio** | **SE** | **Z Ratio** | **p** |
|---|---|---|---|---|
| Cheek / Ear | 1.83 | 0.19 | 5.89 | 0.00 |
| Cheek / Flank | 0.89 | 0.08 | -1.20 | 0.93 |
| Cheek / Forearm | 0.72 | 0.06 | -3.76 | 0.00 |
| Cheek / Rump | 0.85 | 0.08 | -1.78 | 0.54 |
| Ear / Flank | 0.49 | 0.05 | -6.95 | 0.00 |
| Ear / Forearm | 0.39 | 0.04 | -9.46 | 0.00 |
| Ear / Rump | 0.47 | 0.05 | -7.49 | 0.00 |
| Flank / Forearm | 0.81 | 0.07 | -2.46 | 0.13 |
| Flank / Rump | 0.95 | 0.08 | -0.56 | 1.00 |
| Forearm / Rump | 1.18 | 0.10 | 1.94 | 0.42 |

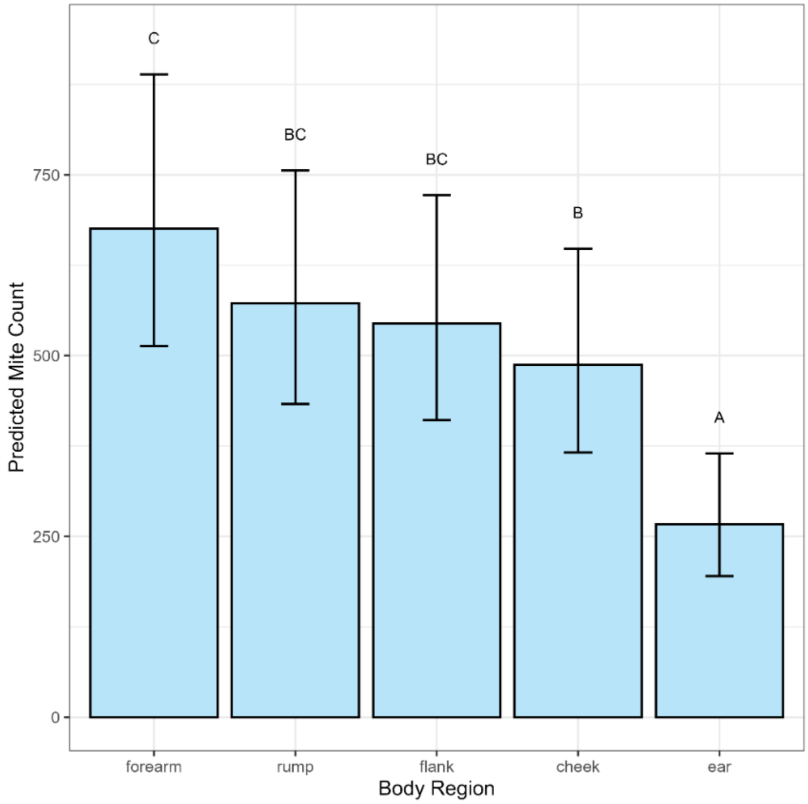

Figure 2.2. Predicted average *Sarcoptes scabiei* burden in one 6 mm biopsy punch for each American black bear (*Ursus americanus*) host body region sampled. Predicted counts are derived from the final model including all mange-positive individuals. Error bars represent 95% confidence intervals. Letters represent pairwise comparison results, with different letters between groups representing significantly different pairs.

## Discussion

Sarcoptic mange has only recently emerged among several black bear populations in the eastern U.S., so understanding the mechanisms of disease progression in the host are critical. This study investigated patterns of mite infestations on bears from three different states where mange is now endemic in bears. Firstly, we found very heavy infestations, with several hundred to thousands of mites present in an area ≤ 20 $cm^3$. This is considerably higher than the previous mite enumeration study by Tiffin et al. (2020), which reported a maximum of 571 mites in similarly sized biopsy samples from bears with severe mange. While the body regions sampled by Tiffin et al. (2020) were not specified and only two bears were included, these discrepancies could point to a wide individual variation in mite burdens, even on animals with notable clinical disease presentation. It is also possible that regional variation exists (samples in the Tiffin et al. study originated from Pennsylvania). Additionally, these very high mite burdens also starkly contrast counts reported in sympatric species. Although high numbers have been reported in some cases (especially in red foxes), anecdotally, we do not tend to see large infestations in submitted wild canids such as coyotes, often leading to difficulty in confirming sarcoptic mange cases (Little et al., 1998; SCWDS, unpublished data); other studies have also noted low mite burdens or difficulty in detections on domestic and wild canids (Curtis, 2012; Tiffin et al., 2025). These differences in levels of infestations could signal a different pathogenesis of sarcoptic mange in bears, including potential differences in hypersensitivity responses between sympatric species.

We were unable to conclude that mite burdens are positively correlated with mange severity in moderately and severely diseased animals, finding no evidence to support the assumption that higher mite burdens are associated with more severe disease outcomes. It is possible that more significant differences would have been noted when compared with mildly diseased individuals, but none were collected in this study. The lack of statistical significance may be attributed to the relatively small sample size used in this analysis. Other studies have sought to employ discrete classification systems to define clinical mange severity, with markers including body condition scores, degree of alopecia, number and characterization of lesions, percentage of skin affected, histologic characteristics, and mite burdens (Kamler & Gipson, 2002*;* Carvalho et al., 2016; DeCandia et al., 2019; Nimmervoll et al., 2013; Pence et al., 1983;

Simpson et al., 2016; Tiffin et al., 2024). However, the results of our work signal that observed mite burden may not be an accurate indicator of disease severity, questioning the use of this metric in clinical evaluations.

Rather than being an indicator of disease severity, it is possible that mite burdens are instead more predictive of the *rate* of disease progression. Davis and Moon (1990) sought to test whether the development of hypersensitivity reactions in swine experimentally infested with *S. scabiei* was dependent on mite densities. Pigs were placed into either a 'low dose' or 'high dose' group based on the number of mites they were infested with. All pigs ultimately progressed through phases of delayed hypersensitivity response; then a combination of delayed and immediate responses; followed by only the immediate hypersensitivity response. However, pigs in the high dose group progressed through these phases more quickly than the low dose pigs, with a faster onset of the initial hypersensitivity response in the high dose pigs (Davis and Moon, 1990). The study was therefore able to conclude that the temporal progression of disease was influenced by mite burden, with faster disease progression occurring with increased burdens. The present study tested mite burden in relation to clinical disease severity on bears and did not find a notable relationship; perhaps in reality, *S. scabiei* burden on black bears is actually influencing time to onset of clinical disease and disease progression rather than severity of clinical presentation. Clinical trials would be necessary to truly explore this hypothesis.

Similar mite burdens in moderately and severely affected groups may speak to the nature of disease development in bears. In canids, which have been noted to have dramatic hypersensitivity responses, low mite burdens are often found on skin scrapings (Little et al., 1998; Niedringhaus et al., 2019a), suggesting that only a small number of mites are required to elicit a large immune reaction and subsequent severe clinical manifestations. Similarly, it is possible that bears only need a certain level of infestation to trigger an immune response that produces more severe clinical signs. Once at this point, disease may naturally progress to the highest severity levels regardless of the number of mites present. Thus, it is possible that severely diseased bears have simply been infested for a longer period of time, and are only being evaluated at the end stage of the disease process.  Studies on the pathogenesis of mange in black bears would be necessary to explore this, including monitoring bears with knowledge of the precise point of infestation, which poses immense difficulties and may only be possible with experimental infection trials.

This line of thought is also interesting when considering the bear host in a landscape ecology context. On the microscale, the bear host can be viewed as the available ‘environment’, and this analysis provides a window into how mites are using their available ‘habitat’. As mites utilize the epidermis on the bear to shelter, feed, survive and reproduce, they may reach a ‘carrying capacity’ wherein the amount of resources that the skin layer can provide is maximized. Thus, we may only see the number of mites increase up to a certain point in the disease process, after which host condition continues to deteriorate but mite burdens do not simultaneously proliferate.

Importantly, we also found differences in mite burdens across various regions of the host body, further advancing our understanding of clinical disease progression and how mites move on the host. Mites were not homogenously distributed on the bear, which could be due to a combination of host and parasite behaviors. Even burdens between all five biopsies taken from a single 6 x 6 cm skin sample were not always similar, further underscoring the extreme variability of mite burdens on the bear. Tiffin et al. (2020) also found variation in mite counts across multiple biopsies sourced from the same lesion on an individual, leading authors to assert that collection of multiple biopsies from the same area on an animal is ideal.

In moderately and severely diseased bears, the highest burdens were typically found on the forearm, rump and flank samples (Figure 2.2). The rump and flank counts were also the most highly correlated to the whole body grand total counts, suggesting that these body regions are the most representative of the overall mite burden on the bear. It is worth questioning if the same patterns would be seen on mildly infested bears at the start of infestation. If differences are noted in these individuals, we may be able to see how the movement of mites on the host relates to mange pathogenesis and epidemiology. Do mites typically colonize a particular area first, then migrate to other parts of the body over time? For example, if we see higher burdens on facial areas in early-stage mild infestations, then observe higher burdens on the rump or flank in late-stage, moderately to severely diseased individuals, we may hypothesize that bears could be contracting mange by eating infested carrion, such that mites first colonize the facial area. This is supported by work in red foxes that has noted the presence of lesions beginning on the ischial region in most cases and suggested that mites have preferred sites on the host (Nimmervoll et al., 2013). Again, these questions can only be definitively answered through studies tracking individuals from beginning to end-stage disease, but our findings of differential mite burdens highlight the need for further explorations.

More clearly, the finding of variably distributed mite burdens carries important implications in terms of bear management, specifically sarcoptic mange monitoring and sampling. The highest mite burdens were found on the forearm, rump, and flank samples, which were also not significantly different from one another. Sampling these areas may therefore best capture true mite burdens, especially the flank and rump, which were most highly correlated to whole body burdens. Although less comprehensive, a single scrape is often the easiest sample to procure in field settings where samples must be obtained quickly and efficiently. The body regions with the highest mite burdens are therefore likely the best places to sample for accurate diagnoses. On the other hand, although the ear may be an easier place to sample from, it tended to have the lowest mite burdens and was unrelated to all other body regions. It is therefore less recommended, as it is least likely to represent true mite burdens and more likely to lead to false negative diagnoses when a single scape is taken. While the skin scrape method is one of the simplest diagnostic methods, we assert that single-use 6 mm biopsy punch digestions are a competitive alternative for biologists. Although longer back-end processing time is required, these samples are small enough to be easily collected from a dead or temporarily immobilized animal (Tiffin et al., 2025), are equally efficient to procure, and have been shown to have higher mite detection sensitivity over skin scrape cytology (Tiffin et al., 2025); they obtain additional mites still buried in the epidermis, which skin scrape samples miss, and therefore can increase diagnostic sensitivity.

Additional analyses should ideally be conducted with more bears from other populations with sarcoptic mange presence to corroborate these findings. More direct comparisons of burdens in other sympatric species in these areas may also be useful to corroborate anecdotal and early findings of higher burdens on black bears (Tiffin et al., 2025), which if true, could point to different disease responses between species. Future work should also incorporate comparisons with individuals experiencing milder infestations, which would improve understanding of early-stage disease dynamics and capture a fuller clinical picture. It is likely that more significant differences in mite burdens would have been observed in comparisons between mildly and severely diseased individuals. The present study intended to collect individuals with mild clinical mange, but no submissions were received. Disease surveillance is typically biased toward nuisance animals, moribund animals and/or those with outward, dramatic disease presentations; also, the animals in this study had to be dead or dispatched to collect sufficient skin. For example, multiple animals in this study were dispatched by wildlife personnel due to a combination of poor physical appearance and exhibition of negative and/or abnormal behaviors (e.g., lingering by roadways, occupying homes or chicken coops, eating agricultural crops, showing aggression or lack of fear), the latter presumably at least in part due to their deteriorated mentation and physical conditions. The lack of collections of mildly diseased individuals may therefore be promising; it is possible that they are still faring well and either escaping detection or potentially overcoming infestations.

In conclusion, this study was able to better characterize the degree and pattern of *S. scabiei* infestation in black bears, noting remarkably high and unevenly dispersed mite burdens in clinically diseased individuals with no associations to level of clinical severity. These findings are important steps towards improved quantification of mange severity and an understanding of sarcoptic mange pathogenesis in the black bear. Our lack of correlation between severity and mite burdens poses implications for how mange in black bears is assessed and monitored, suggesting that mite burden is not always an accurate metric for evaluation of disease severity and should be used with caution. Additionally, we show that sample collection locations should be chosen strategically, as mite counts are variable on different body regions of the host and it therefore does matter where biologists sample from. These results are a critical step towards understanding the drivers behind clinical disease progression of sarcoptic mange in a relatively new host species, and can also facilitate field sample collection to promote simple, standardized, efficacious techniques to improve disease surveillance.

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# CHAPTER III

# SPATIAL TRENDS IN REPORTS OF AMERICAN BLACK BEAR (*URSUS AMERICANUS*) MANGE IN THE OZARK MOUNTAIN REGION, ARKANSAS [2]

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[2] Broadhurst, J.R., Francisco, R., Ballard, J.R., Means, M., Riggs, A. J., Scognamillo, D.G., Haynes, E., Kohl, M.T., and Yabsley, M.J. To be submitted to a peer-reviewed journal.

## Abstract

Sarcoptic mange, caused by the mite *Sarcoptes scabie*i, has contributed to numerous wildlife population health declines in North America, and notably, has recently moved into eastern American black bear (*Ursus americanus*) populations over the last few decades. The reasons for the expansion of this parasitic mite into a new host species are not well understood; consequently, there is a growing effort to understand the potential risk factors predisposing certain bear populations to outbreaks of sarcoptic mange. Spatial studies on other species have shown an uneven distribution of sarcoptic mange on the landscape, with severely affected individuals often deviating from normal behavioral patterns. As black bears can also experience dramatic disease progression, it is reasonable to suspect that they would experience similar impacts to behavior, but no studies have attempted to characterize the spatial distribution of mange in bears. In the Ozark Mountain Region of Arkansas, USA, an outbreak of sarcoptic mange has been occurring within the region's black bear population since 2018. Public reporting data of bears with signs of clinical sarcoptic mange were analyzed to ascertain potential spatial trends in mange reports and examine whether areas with increased development tend to experience more bear mange reports. Using a resource-selection function to study habitat characteristics related to anthropogenic change, it was found that the level of development in an area does influence the probability of reporting a black bear with mange in this region. By predicting where interactions between people and diseased bears are likely to occur, these results can aid in the management of sarcoptic mange on the landscape.

## Introduction

Mitigating disease transmission is at the forefront of animal population management, and understanding the mechanisms behind pathogen spread is paramount to safeguarding population health (Joseph et al., 2013). Managing disease issues in wildlife populations specifically poses unique challenges yet is a critical component for maintaining health at the wildlife-livestock-human interface (Portier et al., 2019). Wildlife diseases can significantly threaten conservation goals for many species and impact ecosystem health; consequently, work to describe the epidemiology, pathology and transmission of wildlife diseases is ever-growing (Joseph et al., 2013; Deem et al., 2001). Particularly, the application of spatial ecology to wildlife disease epidemiology can help identify factors influencing disease transmission and inform how pathogens move on the landscape.

Mange has a near-global distribution and impacts domestic and wild animals across numerous taxonomic groups (Astorga et al., 2018; Pence & Ueckermann, 2002). Mange is a skin condition caused by the infestation of parasitic mites, and affected animals may develop alopecia, severe pruritus, epidermal crusting, hyperkeratosis, and erythema, though clinical manifestations can be variable across species. In wild animals, mange can contribute to significant morbidity and mortality events, impacting population health and conservation efforts. Although >250 mite species can cause mange, *Sarcoptes scabiei*, the causative agent of scabies in humans and sarcoptic mange in animals, is most commonly implicated in cases of clinical disease (Mullen and OConnor, 2019). Sarcoptic mange is globally distributed across six continents and in over 100 mammalian species belonging to at least 12 taxonomic orders (Niedringhaus et al., 2019a; Escobar et al., 2022). *Sarcoptes scabiei* is a burrowing mite that tunnels into the stratum corneum of the epidermal layer of the host’s skin, leading to skin lesions and the aforementioned clinical signs. In severe cases, the associated lesions can result in secondary fungal and bacterial infections, emaciation, anorexia, dehydration, and eventual death (Currier et al., 2011; Niedringhaus et al., 2019a; Bornstein et al., 2001). Thus, an understanding of *S. scabiei* dispersal and sarcoptic mange distribution are crucial to mitigate threats to human and animal health.

In North America, canids have been disproportionately affected by sarcoptic mange (Niedringhaus et al., 2019a), comprising the majority of the enzootic events observed in this region. The American black bear (*Ursus americanus*) was not historically adversely affected by mange, yet over the last few decades, *S. scabiei* has emerged as a potential threat to North American bear populations (Niedringhaus et al., 2019a). The first documentation of sarcoptic mange in a North American black bear was recorded in Michigan in 1987 (Schmitt et al., 1987). To date, mange has been detected in several other states at endemic or emerging levels (Niedringhaus et al., 2019b) with continued geographic spread anticipated. The driving forces behind the emergence of this parasite in a new host species, however, are not well understood. Many factors have been theorized, including host and parasite genetic characteristics, co-infections, anthropogenic disturbance, geographic spread of the parasite, and spatial population dynamics of the host; however, no definitive contributing factor has been identified (Niedringhaus et al., 2019b; Peltier et al., 2017).

Although no published works currently exist for black bear hosts, recent studies have sought to characterize spatiotemporal trends and potential anthropogenic influences behind sarcoptic mange distribution and how this affects animal movement and behavior. Several studies, primarily in canid species, have found positive associations between sarcoptic mange prevalence and urban development as well as fluctuations in home range sizes (Carricondo-

Sanchez et al., 2017; Cypher et al., 2023; Murray et al., 2015b; Murray et al., 2021; Murray & St. Clair, 2017), underscoring the marked energy deficits imposed by mange and its ability to drastically change behavioral and movement patterns. As this disease has only recently emerged in black bears, similar studies attempting to characterize the spatial patterns behind its distribution in bear populations are lacking.

The objective of this study was to explore potential spatial trends in reports of black bear mange cases within the Ozark Mountain Region, Arkansas, USA, a population experiencing the emergence of sarcoptic mange. After near extirpation due to habitat loss and overharvest in several portions of their range in the state by the early 1900's, bears sourced from Minnesota and Manitoba, Canada were successfully reintroduced into the Ozark Mountain Region beginning in 1958 (Kristensen et al., 2019). Sarcoptic mange was first reported in the Ozark Mountain population in 2018, and these bears have been experiencing endemic levels of mange since then, allowing for the examination of the very recent emergence of sarcoptic mange in a relatively new and isolated population with a known health history. The Ozark Mountain black bears therefore serve as an ideal population to examine the influence of environmental and anthropogenic factors on the presence of sarcoptic mange. Additionally, a mix of national forest, privately owned human settlements, and growing development interspersed throughout the study area provides the ability to examine spatial relationships across a gradient of urbanization. A resource-selection function (RSF) model was employed to analyze reports of bear mange and explore covariates related to increased urbanization, including distance to various anthropogenic structures, land cover types, and population densities in reporting locations. Due to positive associations observed in other species (e.g., Carricondo-Sanchez et al., 2017; Murray et al., 2021), we predicted that bear mange reports would be positively correlated with higher levels of urbanization. Identifying such relationships would provide critical information on the spatial attributes of locations with bear mange outbreaks and thus allow wildlife managers to concentrate management efforts in the areas of greatest concern.

## Methods

### *Study Area*

We used reports of sarcoptic mange in black bears from a 39,828 km$^2$ area of the Ozark Mountain Region of Arkansas, USA for this analysis. The northern and western bounds of the study area were demarcated based on Arkansas state lines (Figure 3.1). The southern boundary ran along the Arkansas River, just past interstate I-44 (Figure 3.1). The eastern boundary was drawn following the Ozark Highlands, Boston Mountains, and Arkansas Valley ecoregions (Woods et al., 2004).

The region has a high diversity of topographic features, including mountainous areas with heavy evergreen, deciduous and mixed forests, valleys containing plains, hills, and wooded areas, plateaus, and cleared areas for pastureland, hay land and cropland (Woods et al., 2004). Thus, the area contains a mix of extensive forested areas acting as important bear habitat with scattered agricultural and urban developments. The Ozark St. Francis National Forest is situated in the southwestern portion of the study area (Figure 3.1) and contains the greatest amount of contiguous forest with various developments and fragmented forest areas surrounding this space. The study area contains both public and private ownership, with federally managed forest and private residences and farmland scattered throughout.

Figure 3.1. The Ozark Mountain Region in northwestern Arkansas, USA included in the current study. The black outline represents the Arkansas state boundary. The red outline denotes the study area boundary.

*Reporting Data*

The Arkansas Fish and Game Commission (AFGC) collected reports of mange cases in black bears from February 2018 to September 2022. These included reports of observations of bears with visible mange symptoms from the public and/or state wildlife agency personnel.

Demographic information for each animal included age group, sex, ear tag or collar, and a description of the case, when available. Other recorded information included the date of the report, case type (e.g., suspect mange case, den check, etc.), county, UTM coordinates, description of the location, biological samples collected, treatment administered, and other case notes.

For several cases, precise location data were not recorded with reports. In cases where geographic coordinates were missing but approximate location information was provided (i.e. street addresses, roads, landowner names) in the location description and case notes, we estimated spatial coordinates in Google Earth (Google, Mountain View, CA) and Bing Maps (Microsoft, Redmond, WA). When only vague location descriptions were recorded (i.e. near a town; in the direction of a mountain or geographic feature), we censored cases from the data.

### *Spatial Explanatory Variables*

We quantified the levels of anthropogenic disturbance through various spatial metrics that included distance to roads, percent urbanization, percent forest cover, human population density and a proxy for bear density based on habitat suitability indices. We obtained land cover data to determine amounts of urbanization and forest cover from the 2021 USGS National Land Cover Database (NLCD). From this, we estimated % forest by combining all NLCD forest cover types and applying a 3x3 focal moving window using the Focal Statistics tool in ArcGIS Pro version 3.2.1 (ESRI, 2023). We applied the same process to calculate percent urbanization, using all categories of developed land (i.e., high, medium, low development). We obtained road data from the Arkansas GIS Office Centerline File and calculated Euclidean distance to roads using the Euclidean Distance tool in ArcGIS Pro version 3.2.1 (ESRI, 2023). We estimated human population density from the 2023 U.S. Census Bureau tabulation block data by dividing the population count by the land area provided within the Census Bureau block data.

To provide a representative index of bear density, we obtained a previously developed black bear habitat suitability index that included our study area (Glymph, 2017). This metric was of importance as evidence for density-dependent sarcoptic mange transmission has been observed in some systems; it is also thought that more urbanized areas can facilitate atypical increases in contact between individuals of a population (Almberg et al., 2012; Carricondo-Sanchez et al., 2017; Cypher et al., 2023; Sommerer, 2014; Uraguchi et al., 2014). In the previous study, a Maxent machine learning model was used to model habitat suitability at a 30-meter resolution. Known black bear presence points were analyzed alongside relevant environmental predictor variables to predict areas of suitable habitat. For our analysis, we assumed that bear density would be positively correlated with habitat suitability.

### *Modeling*

We estimated mange distribution across the study area using a resource selection framework at the second order (Manly et al., 2002). To identify potential mange cases (i.e., available locations), we systematically sampled points at a magnitude of approximately ten times the number of reports, using 30-meter resolution spatial data. We used the st_sample function (with type = “regular”) from the sf package in Program R for sampling (version 4.4.3, R Core Team 2023). We then estimated the probability of observing a bear mange report given the spatial characteristics at a specific location by fitting generalized linear models with a binomial distribution as a function of the aforementioned covariates.

We assessed model fit from a model suite that included all-possible additive combinations of standardized spatial covariates. Interactive effects were not tested due to small sample size. Linear and quadratic functional forms of the relationships were tested to assess any nonlinearities and compared for better fit through raw data plot visualizations and Akaike Information Criterion (AIC) scores. We treated all variables as continuous and examined for collinearity using Pearson’s correlation (all $\leq 0.4$). We evaluated model fit using AIC scores adjusted for small sample sizes. To account for model uncertainty, we employed full model averaging across candidate models within Δ7 AIC ($n = 6$) using the MuMIn package in Program R. Model-averaged predictions were then generated. We performed all analyses using Program R (version 4.4.3, R Core Team 2023).

## Results

We recorded a total of 69 reports that met our inclusion criteria (i.e., sufficient location data and evidence of clinical mange in case descriptions) from 2018 to 2022. The distance to roads, human population density, percent forest cover and percent urbanization covariates all showed nonlinear relationships based on raw data plots and better performance in AIC rankings. These were therefore included as quadratic terms in the global model. The bear habitat suitability covariate was best explained by a linear term in the global model (Table 3.1). The distance to roads, percent urban, percent forest and bear habitat suitability covariates also showed statistical significance ($p < 0.05$) and some degree of predictive power over the null model as univariate models (Table 3.1). The best performing models ($n = 6$) collectively included combinations of all covariates (Table 3.2).

Table 3.1. Model weights for the generalized linear model candidates tested to predict the probability of black bear mange reporting in the Ozark Mountain Region of Arkansas, USA from 2018-2022. The models in this table include a null model, univariate models for each covariate represented as both linear and quadratic terms, and a global model. $^2$ indicates the quadratic form of the variable (linear term + squared term).

| **Model** | **K** | **AICc** | **ΔAICc** | **AICc Wt** | **Cum. Wt** | **LL** |
|---|---|---|---|---|---|---|
| Global | 10 | 434.72 | 0.00 | 0.83 | 0.83 | -205.46 |
| % Urban$^2$ | 3 | 437.96 | 3.23 | 0.17 | 1.00 | -215.79 |
| Distance to Roads$^2$ | 3 | 446.52 | 11.80 | 0.00 | 1.00 | -220.08 |
| % Urban | 2 | 453.17 | 18.44 | 0.00 | 1.00 | -224.49 |
| Distance to Roads | 2 | 460.79 | 26.07 | 0.00 | 1.00 | -228.30 |
| % Forest$^2$ | 3 | 468.56 | 33.84 | 0.00 | 1.00 | -231.09 |
| Bear Habitat Suitability | 2 | 471.26 | 36.54 | 0.00 | 1.00 | -233.54 |
| Bear Habitat Suitability$^2$ | 3 | 473.45 | 38.73 | 0.00 | 1.00 | -233.54 |
| % Forest | 2 | 474.23 | 39.51 | 0.00 | 1.00 | -235.03 |
| Null | 1 | 474.25 | 39.53 | 0.00 | 1.00 | -236.09 |
| Population Density | 2 | 475.54 | 40.82 | 0.00 | 1.00 | -235.68 |
| Population Density$^2$ | 3 | 477.73 | 43.01 | 0.00 | 1.00 | -235.68 |

Table 3.2. Model weights for the top generalized linear models used in model averaging to predict the probability of reporting black bear sarcoptic mange in the Ozark Mountain Region of Arkansas, USA from 2018-2022. $^2$ indicates the quadratic form of the variable (linear term + squared term).

| Model | K | AICc | ΔAICc | AICc Wt | Cum. Wt | LL |
|---|---|---|---|---|---|---|
| Distance to Roads$^2$ + % Urban$^2$ + Bear Habitat Suitability | 6 | 426.17 | 0.00 | 0.48 | 0.48 | -207.03 |
| Distance to Roads$^2$ + % Urban$^2$ + Population Density$^2$ + Bear Habitat Suitability | 8 | 427.28 | 1.11 | 0.28 | 0.76 | -205.55 |
| % Urban$^2$ + Bear Habitat Suitability | 4 | 429.40 | 3.23 | 0.10 | 0.85 | -210.68 |
| Distance to Roads$^2$ + % Forest$^2$ + % Urban$^2$ + Bear Habitat Suitability | 8 | 430.09 | 3.92 | 0.07 | 0.92 | -206.96 |
| % Urban$^2$ + Population Density$^2$ + Bear Habitat Suitability | 6 | 431.14 | 4.97 | 0.04 | 0.96 | -209.52 |
| Global | 10 | 431.20 | 5.03 | 0.04 | 1.00 | -205.46 |

The additive generalized linear averaged model included all covariates, but suggests that there are particularly strong effects of distance to roads, percent urbanization and bear habitat suitability on the probability of experiencing a report of bear mange (Table 3.3). When very close to roads as well as at larger distances to roads, the probability of observing a bear mange report within the study area increases (Figure 3.2a). In relation to percent urbanization, the probability of reporting a case is highest at intermediate levels and decreases in areas with very low and very high urbanization (Figure 3.2b). Finally, there is a direct positive relationship between the probability of experiencing a bear mange report and bear habitat suitability (Figure 3.2c).

Table 3.3. Parameter estimates for the final generalized linear model based on reports of sarcoptic mange in black bears (*Ursus americanus*) in the Ozark Mountain Region, Arkansas, USA. 95% confidence intervals are shown

| **Variable** | **Estimate** | **Std. Error** | **Lower CI** | **Upper CI** |
|---|---|---|---|---|
| Intercept | -2.67 | 0.25 | -3.15 | -2.18 |
| Distance to Roads (linear) | -0.58 | 0.33 | -1.17 | -0.16 |
| Distance to Roads (squared) | 0.14 | 0.08 | 0.03 | 0.29 |
| % Urban (linear) | 1.00 | 0.29 | 0.44 | 1.56 |
| % Urban (squared) | -0.20 | 0.09 | -0.38 | -0.02 |
| Bear Habitat Suitability (linear) | 0.42 | 0.14 | 0.15 | 0.69 |
| Population Density (linear) | -0.21 | 0.41 | -1.57 | 0.38 |
| Population Density (squared) | 0.01 | 0.03 | -0.06 | 0.11 |
| % Forest (linear) | 0.00 | 0.08 | -0.53 | 0.47 |
| % Forest (squared) | 0.01 | 0.09 | -0.50 | 0.60 |

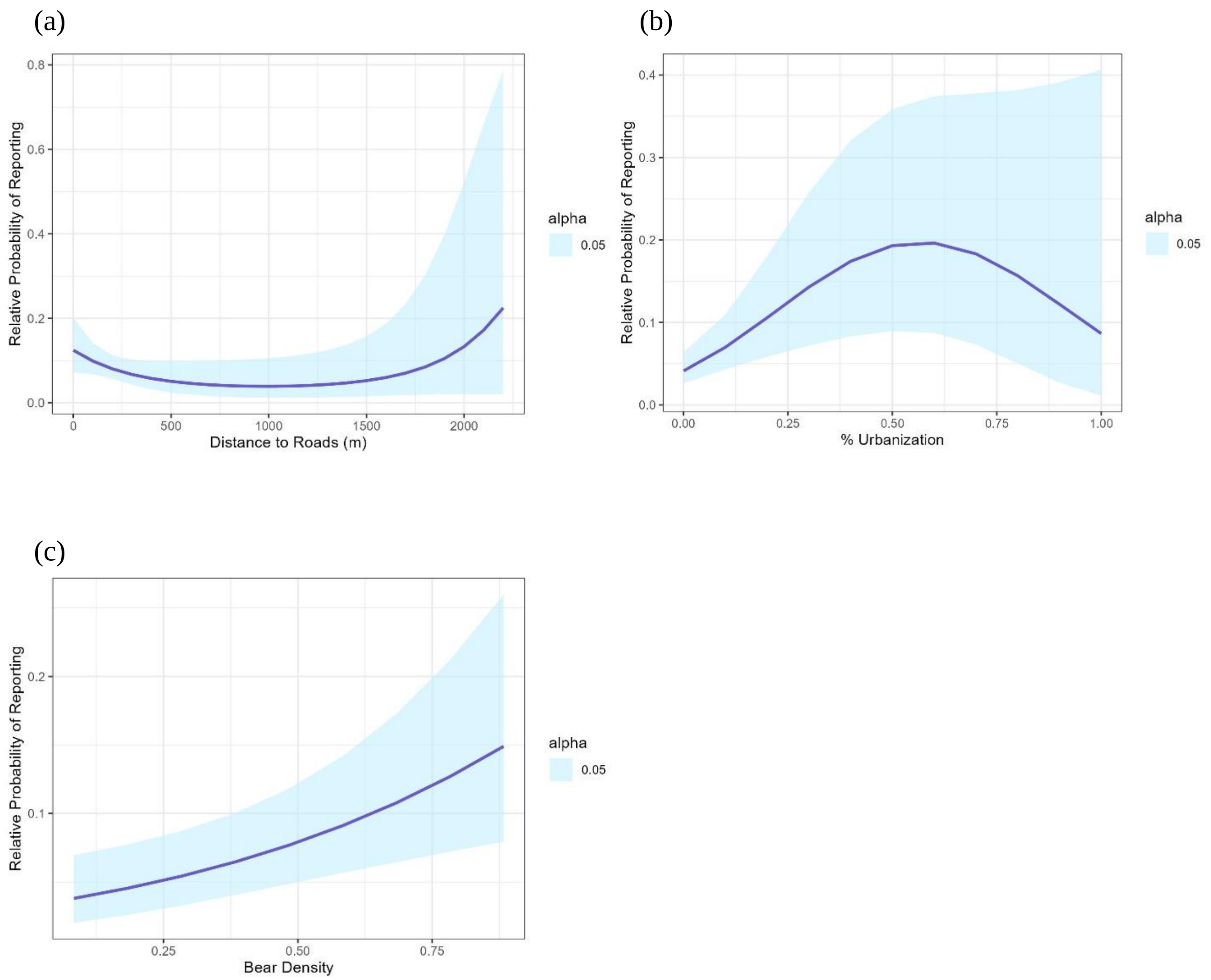

Figure 3.2. The relative probability of reporting a black bear (*Ursus americanus*) with mange in the Ozark Mountain Region of Arkansas based on (a) distance to roads, (b) percent urbanization and (c) bear habitat suitability. Axes reflect values from standardized variables. Lines represent fitted values with 95% confidence intervals represented by shaded areas from the averaged generalized linear model.

## Discussion

The Ozark Mountain Region black bears serve as an ideal population to examine the influence of environmental and anthropogenic factors on the presence of sarcoptic mange. We examined the recent emergence of sarcoptic mange in an isolated population across a gradient of urbanization. Based on the results of this analysis, it does appear that the degree of anthropogenic alteration in an area does influence the likelihood of reporting a bear with mange. Consequently, this may assist in informing where best to concentrate management activities, mitigation efforts, and public education by elucidating areas that are most likely to facilitate encounters between people and bears with sarcoptic mange.

Understanding sarcoptic mange transmission is of utmost importance due to its nearly global distribution and continued expansion into novel hosts and environments (Escobar et al., 2021). Across other species, and in particular canids, individuals with sarcoptic mange tend to stray from their normal space use patterns. Studies on red foxes (*Vulpes vulpes*) and coyotes (*Canis latrans*) have reported that animals with apparent clinical mange were more likely than healthy conspecifics to be located near human settlements and to occupy residential habitats, especially in winter months (Carricondo-Sanchez et al., 2017; Wilson, 2012). Another study modeling the estimated occurrence of mange in coyotes also found that individuals with mange were more likely to occupy low-density urban development areas than healthy individuals (Murray et al., 2021); in some cases, coyotes in urban environments also experience higher mortality rates due to mange compared to affected individuals in rural environments (Gosselink et al., 2007). Similar findings and reductions in movement have even been reported in wombats, another species group that is highly afflicted by mange (Ringwaldt et al., 2023; Simpson et al., 2016). For example, potential landscape and host-associated variables predictive of mange in Tasmanian bare-nosed wombats (*Vombatus ursinus*) were evaluated; although mange was widespread, its presence was not evenly distributed on the landscape (Ringwaldt et al., 2023). In addition to other environmental variables such as distance to water sources or topographic roughness, mange reports were more probable in croplands and other areas with increased anthropogenic disturbance (Ringwaldt et al., 2023). Consequently, these spatial and behavioral shifts have the potential to exacerbate human-wildlife conflicts, especially in urban areas (Wilson, 2012).

Other changes to animal behavior and movement patterns associated with mange infestation have also been noted. While little to no published works exist addressing black bears, a recent thesis by Tiffin (2022) found that bears with severe sarcoptic mange exhibited lower average step lengths and decreased activity levels. In wolves with mange, thermal cameras revealed that diseased individuals suffered from increased heat loss, thus resulting in significant energy costs (Cross et al., 2016). Notably, one infested individual even shifted its activity to follow an unusual diurnal pattern, highlighting the possibility that mange-induced thermal energy loss may require animals to shift diel activity patterns entirely (Cross et al., 2016). Similar behavioral trends have been noted in coyotes with mange, which appeared to be more active during the day than other healthy coyotes in an urban environment (Murray et al., 2015b). Infested wolves also traveled increasingly less distance per day compared to healthy wolves as their mange severity increased (Cross et al., 2016). Similar findings have been reported for San Joaquin kit foxes (*Vulpes macrotis mutica*), raccoon dogs (*Nyctereutes procyonoides*), and Ibex, with diseased individuals moving less than their healthy counterparts and experiencing shrinkages of home range size (Cypher et al., 2023; Perez et al., 1997; Süld et al., 2017). Other observations have included increased scavenging, extended periods of inactivity, lack of appropriate fear of humans, decreased dispersal rates, and the use of abnormal denning sites (*Morphology, Reproduction, Dispersal, and Mortality of Midwestern Red Fox Populations*, n.d.; Shelley & Gehring, 2002; Trainer & Hale, 1969; Wydeven et al., 2003). These studies exhibit the marked energy deficits imposed by mange, and its ability to drastically change behavioral and movement patterns (Cross et al., 2016; Shelley & Gehring, 2002). However, other studies have noted no differences in home range sizes (Kamler & Gipson, 2002; Chronert et al., 2007), highlighting the complexity and stochasticity of sarcoptic mange and its impacts on wildlife populations. Still, well-documented patterns in other mange systems do exist and lend credence to our findings of bear mange reports being associated with anthropogenic variables.

It has been hypothesized that increased prevalences of mange are present in areas of higher anthropogenic alteration in part due to easier access to resources in these environments. As an animal's energy capacity and overall health declines in response to mange, readily available human food resources or the availability of anthropogenic structures such as abandoned buildings for shelter become more attractive, thereby also increasing the likelihood of human-wildlife encounters (Carricondo-Sanchez et al., 2017; Murray et al., 2015b; Murray & St. Clair, 2017; Reddell et al., 2021). Conversely, abundant human food availability in urban areas may facilitate unnatural congregations or overlapping home ranges of animals (Carricondo-Sanchez et al., 2017), increasing the likelihood of direct pathogen transmission or heightening individual stress responses that increase vulnerability to infection. Since black bears likely demonstrate similar disease progression to other wild mammals, future work should investigate if these behavioral trends are also present in bears. While our study cannot escape reporting bias to investigate true resource selection patterns, our results do coincide with other spatial studies and may therefore have true underlying biological significance. Additionally, it is worth acknowledging that although the previous research has provided valuable insight into potential mechanisms for disease spread, many results have been limited to information gathered by remotely triggered wildlife cameras, which may lead to imprecise or underestimated disease detections (Murray et al., 2021; Reddell et al., 2021). Examination of reporting data offers an alternative way to track and model spatial disease occurrences and can complement and augment traditional camera trap data.

In a study by Saito et al. (2017) of racoon dogs with sarcoptic mange along an urban gradient, the highest probability of occurrence of symptomatic racoons was observed in non-forested and intermediate forest landscapes, leading to the conclusion that urban and suburban areas held higher densities of animals. In Chicago, coyotes with mange were more likely to occur in urban areas with low housing densities and higher canopy cover (Murray et al., 2021). In that study, it was hypothesized that these areas were more attractive to coyotes with mange due to their propensity to scavenge anthropogenic food resources rather than hunt, while still offering vegetative cover (Murray et al., 2021). Similar to those studies, we found that the highest probability of a bear mange report occurred at intermediate levels of urbanization. More sightings of diseased bears in these areas, as opposed to in areas with higher urbanization and likely more people, could signal that bears with clinical mange do select for areas with increased urban development as their abilities to survive and forage diminish, but that the most highly urbanized areas still do not provide suitable habitat.

Conversely, analyses of reports by proximity to roads showed higher probabilities of reporting mange cases at both the closest and furthest distances from roadways, with a decrease in probability of reporting mange at intermediate distances. Thus, it is possible that most people are likely to report sightings either while driving or in areas with less congestion and impervious surfaces. It is possible that a subset of bears experiencing late-stage, severe disease outcomes may be utilizing roadways as corridors to facilitate ease of movement, as has been observed in other species (Shelley & Gehring, 2002), which could explain the increased probability of reporting a case at these close distances in some instances. Diminished cognitive and physical capabilities in these severely infested animals could also make them more likely to travel into otherwise risky spaces despite increased potential for road mortality. However, these findings may simply be a product of reporting biases (Soulsbury et al., 2007). Under the assumption that increased impervious surfaces and associated habitat losses likely lead to higher congregations of individuals, a thesis by Sommerer (2014) hypothesized that increases in impervious land cover are positively associated with increased bear mange occurrence in Pennsylvania; however, it was concluded that no association between impervious land cover and bear mange existed. While we did find a significant relationship in bear mange reports as a function of distance to roadways, it is unclear whether these results are truly contradictory to the Pennsylvania study or instead a function of human reporting bias.

Utilizing habitat suitability indices as a proxy for bear density in the study area, we identified a clear positive correlation between bear habitat suitability and reporting, with higher probabilities of reporting bear mange occurring in areas of higher habitat suitability. Reports being likely correlated with bear prevalence represents a promising trend that suggests potential for a true relationship outside of the reporting biases inherent in our study. To date, very few studies have evaluated the impact of sarcoptic mange on the home range or spatial movements of black bears. However, given the disease's documented negative health impacts and the similar clinical signs among many species considered, it is reasonable to expect that mange would lead to deviations from normal movement and behavior in black bears. Additionally, as a species that is already involved in many cases of human-wildlife conflict (Don Carlos et al., 2009; Homstol et al., 2024), it would not be surprising to see an increase in these interactions as disease weakens host mentation and physical condition while simultaneously causing highly visible signs likely to catch the attention of people.

While the reliance on public reporting data in this study limits our ability to ascertain definitive habitat selection trends, the true power of these results is instead in their ability to enlighten understanding of human-wildlife interactions, where and how the public engages with diseased wildlife, and how wildlife professionals can best tailor management and education actions. As coexistence between people and wildlife grows increasingly challenging in the wake of increased contact and shared spatial resources, understanding the nuances of these interactions and where conflict is likely to occur is critical for the application of strategic mitigation efforts in key areas (Merkle et al., 2011; Murray et al., 2015b). In some instances, animals exhibiting conflict-prone behaviors in urban settings have even been shown to have a higher likelihood of exhibiting clinical mange infestation (Murray et al., 2015a), further underscoring this need. Citizen science has been effectively employed to record and monitor sarcoptic mange in wildlife (Mayadunnage et al., 2024; Scott et al., 2020; Soulsbury et al., 2007); the utilization of public reporting data here and in other recent studies represents an interesting way to both spatially track wildlife diseases and pinpoint conflict-prone areas.

In a study modeling the probability of human-bear interactions (HBI), different management strategies based on the likelihood of HBI were proposed, including educational programs to increase knowledge and awareness in areas with low HBI probability, and combinations of both educational programming and ordinances to negate antagonistic human activities in high-probability HBI areas (Merkle et al., 2011). These same principles can be applied to issues involving human interaction with diseased bears. This is especially relevant in the case of a zoonotic disease such as sarcoptic mange, where interactions can pose both a human and animal health risk.

Future studies should ideally entail additional surveillance methods (i.e., camera trap data and radio-collared animals) to help confirm the suspected ecological reasonings behind these results. Additional surveillance should also be conducted to increase the small sample size available in this study and ultimately bolster the strength of these predictions. While much more work is necessitated to understand the emergence and persistence of sarcoptic mange in this population and the spatial trends behind its spread, this study provides evidence that anthropogenic disturbance and development play an important role in the increase of public interaction with mange-infested black bears. There are other possible explanatory factors that could be at play, including differences on private versus public lands, or distances from riparian and recreation areas. The framework constructed for this model can accommodate additional covariates such as these and pave the way for further exploration. These results highlight the need for more investigation into the role of urban environments in sarcoptic mange transmission and overall animal disease spread.

Sarcoptic mange is one of the most widespread and taxonomically indiscriminate diseases on the landscape (Escobar et al., 2021), and its continued expansion and persistence in a variety of animal populations has significant management implications. With its ability to parasitize hundreds of mammalian hosts, including humans, it presents true risk to public and ecosystem health. Ultimately, this work has the potential to inform where to concentrate mitigation efforts and predictions of likely areas of future outbreaks. Considering the relatively recent appearance of mange in North American black bears, more work is necessary to understand the drivers behind its spread and the associated potential dangers to bear, human, and ecosystem health. It is hoped that these findings provide a foundation for subsequent work and prove valuable in helping wildlife managers mitigate human-wildlife conflict and risks to public and animal health.

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# CHAPTER IV

# CONCLUSIONS

Sarcoptic mange, caused by the *Sarcoptes scabiei* mite, is a zoonotic parasitic disease of concern for a plethora of mammalian species across the world. As the *S. scabiei* mite burrows into the skin of the affected host to survive, feed and reproduce, associated dermal trauma and host immune responses can lead to severe pruritus, alopecia, skin crusting, hyperkeratosis, erythema and hyperemia. This prolonged discomfort often results in cachexia, dehydration, weakness, and eventual death. With hundreds to thousands of cases in people every year, frequent outbreaks in domestic and companion animals, and regular epizootic events in wildlife populations, it is truly a disease of human, veterinary, agricultural and ecological importance.

Often posing risk to population health and viability, sarcoptic mange is especially problematic in wild animals and remains a challenge for wildlife managers. Historically, North American sarcoptic mange outbreaks were mainly restricted to canids including coyotes (*Canis latrans*), gray wolves (*Canis lupus*), and red foxes (*Vulpes vulpes*). For reasons still largely unknown, however, the American black bear (*Ursus americanus*) has become a commonly affected host within the last few decades. To continue exploration of this actively emerging phenomenon, this research covered two very different but related questions; the main foci were to better understand this emerging disease system by both an analysis of black bear sarcoptic mange distribution on the individual bear host and on the landscape.

The first research chapter of this work characterized *Sarcoptes scabiei* mite burdens on black bears, addressing questions regarding mite quantities on bears, how levels of infestation impact clinical disease severity, and how mites are distributed across different body regions of the host to inform sample collections. Incredibly high mite counts were found on bears with moderate to severe clinical presentations, underscoring the great impact that this disease can have on the host. Despite assumptions, it was also found that mite burdens were not predictive of clinical disease severity. This is an important piece of information towards understanding of sarcoptic mange disease progression in bears, and could be related to the pathogenesis of black bear mange, although this is still unclear. This result also calls into question the current usage of parasitic load as a descriptor of disease severity and potentially suggests the need for a change in methods used to monitor mange in wildlife populations. However, the sample size in this study was small and did not include bears with subjectively mild disease, so future work should include additional bears from more geographic regions to corroborate this finding.

Additionally, it was found that mites are not homogenously distributed on the host body, and significant differences in burdens were quantified on different regions of the bear. Among common sample collection sites, the highest numbers of mites were typically found on the forearm, flank and rump, with lesser burdens on areas of the head including the cheek and ear. These results have important implications for sample collection; sampling from the sites with the highest burdens is likely preferable to have the best chance of identifying mites and thus maximizing accurate diagnoses. It would be interesting to explore if these findings hold true in mildly diseased bears and whether more significant variation in mite burdens between body regions would be seen, which would better capture early-stage disease dynamics. Investigations of mildly diseased and subclinical bears would also help inform the full suite of potential disease outcomes, as it is possible that these bears are able to recover or exist with low-level infestation.

This study highlights the necessity for further work to characterize the pathogenesis of mange in this species.

To evaluate potential spatial trends in black bear sarcoptic mange, the second study investigated the associative value of landscape factors for locations of public bear mange reports within the Ozark Mountain Region bear population in Arkansas. While correlations between anthropogenic development and sarcoptic mange have been noted in other species, limited work has been conducted to characterize similar spatial trends in bears. By analyzing the level of development in the study area with variables including distance to roadways, land cover types, and human and bear population densities, it was found that these metrics of development were correlated with the probability of a bear mange report occurring. Especially strong relationships were noted with distance to roads, percent urbanization, and bear habitat suitability measurements, with the probability of reporting bear mange highest at: closest and furthest distances from roads, intermediate levels of percent urbanization, and increasing bear densities. These findings indicate that, at least through the lens of human-wildlife coexistence, urban development and anthropogenic change may be important factors in the distribution of sarcoptic mange in bears on the landscape.

This research is the first study to utilize public reporting data to spatially examine bear mange presence, intertwining analysis of public and wildlife interactions with syndromic surveillance data to elucidate areas where we may likely see more diseased bears. These results carry important management implications, revealing areas where human-bear interactions and even zoonotic transmission events may be likely to occur. Findings can be used to strategically direct public education campaigns and other management actions to key locations, improving sarcoptic mange mitigation strategies. To further characterize mange distribution in this population, future work should employ camera and collar data to explore how mange may be impacting bear movement and behavior. The framework used herein can be easily expanded to include other spatial covariates of potential interest, which may include proximity to riparian areas, densities of sympatric species, presence on public vs. private lands, and more. These methods may be adapted to conduct similar analyses in other bear mange populations, or even to explore dynamics of other diseases in wild populations.

This body of work explored the presence of *S. scabiei* on the landscape in a twofold manner: first on the microscale as it relates to the bear 'landscape' used by *S. scabiei mites* on the host, and secondly in the context of the host-pathogen spatial environment. As sarcoptic mange continues to spread in eastern U.S. black bear populations, these results assist in a larger effort to better understand this disease to proactively mitigate further population-level impacts. As black bears endure other pressures including habitat losses and human conflict, the potential interactive effects of novel disease introductions are essential to understand. As a well-loved game species with important ecological roles in their environment, research to improve population health is warranted and highly critical.

*S. scabiei* is one of the most successful parasites in history by numerous metrics: its geographic spread, adaptability to a plethora of hosts, impressive virulence, zoonotic potential and centuries-long persistence propels sarcoptic mange to its status as one of the most impactful disease issues worldwide. It is a fascinating parasite: one microscopic mite with the power to enact hugely macroscopic alterations to community health and ecological systems for our wildlife on a global scale. Zooming into the black bear, this work covers only a small portion of this parasite's reach, but it is hoped that these findings can play a part in better managing this globally distributed and spreading disease challenge while also helping to safeguard black bear population health.