JZWM2021 52(1):200-205

[**SPECIFIC MOLECULAR DETECTION OF PIROPLASMS AND CHARACTERIZATION OF β-TUBULIN FOR A NOVEL *BABESIA* SPECIES IN SIKA DEER (*CERVUS NIPPON YESOENSIS*)**](https://doi.org/10.1638/2020-0110)

Mohamed Moustafa MA, Anders JL, Ahmed Mohamed WM, et al

**ABSTRACT:** Piroplasms, which include *Babesia* spp. and *Theileria* spp., are protozoan parasites carried by ticks and commonly cause disease in animals and humans. Those caused by *Babesia* spp. manifest as fever, anemia, and hemoglobinuria, while *Theileria* spp. can lead to high fever, diarrhea, and lymphadenopathy. Recently, *Theileria capreoli* and an undescribed *Babesia* sp. were detected for the first time in sika deer (*Cervus nippon yesoensis*) from Hokkaido; however, there is limited information available on their epidemiology in Japan. Here, a touchdown polymerase chain reaction and reverse line blot hybridization were used to perform an epidemiological survey of *T. capreoli* and *Babesia* sp. using blood samples from 82 sika deer in Hokkaido, Japan. This was followed by partial sequencing and phylogenetic analysis of the 18S rRNA and β-tubulin genes to characterize both piroplasm species. A total of 43 (52.4%) and 3 (3.7%) of the sika deer were positive for *T. capreoli* and *Babesia* sp., respectively. The β-tubulin gene partial sequences for *Babesia* sp. were distinct from those of *Babesia* spp. in GenBank. Phylogenetic analysis showed that the unknown *Babesia* sp. is more closely related to *B. bigemina* and *B. ovata* than other *Babesia* spp. based on the β-tubulin gene. Further studies are required to understand the ecology of these tick-borne pathogens in Japan

**Key Points:**

* Sika deer are native throughout Japan and act as reservoir hosts for many piroplasms
	+ They often live near livestock, increasing the possibility of mixed/multiple piroplasm infections
	+ Sika deer were culled for nuisance control between 2010-13 in Japan
	+ Blood was collected from the jugular vein of 82 sika deer after euthanasia
* Reverse line blot hybridization can detect several tick-borne pathogens with high specificity at a reasonable price
* All *Babesia sp.* positive blood samples were co-infected with *T. capreoli*
* Prevalences of *T. capreoli* and *Babesia sp.* were lower than previously reported
	+ Previously, the higher prevalence of *Theileria* sp. Thrivae and *B. divergens*-like may have affected the detection of *T. capreoli* and *Babesia sp.* due to unspecific universal primers to detect piroplasms
	+ The relatively high prevalence of *T. capreoli* could be attributed to the high abundance and diversity of competent tick hosts in comparison with *Babesia sp.*
* Although the prevalence of *T. capreoli* was high, all animals tested were apparently healthy when culled
	+ Wildlife are frequently found to be asymptomatic carriers for piroplasms especially in endemic areas due to inverse age resistance

**TLDR:** Sika deer have a high prevalence of *T. capreoli* and act as reservoir hosts for many piroplasms in Japan

**Related Articles:** *None on the current ACZM reading list*

JWD 2020 56(4):815-822

[**TICKS PARASITIZING THE SPUR-THIGHED TORTOISE (*TESTUDO GRAECA*) POPULATION OF TUNISIA**](https://doi.org/10.7589/2019-09-219)

Najjar C, Kaabi B, Younsi H, Petretto M, Riordan P, Zhioua E

**ABSTRACT:** From March to April 2017, a total of 147 free-ranging spur-thighed tortoises (*Testudo graeca*) was captured in different habitat types of northern Tunisia and examined for tick infestation. A total of 134 was infested, yielding an infestation prevalence of 91.2%. From these tortoises, 1,174 ticks were collected, a subsample (10%, *n*=120) of which was randomly selected and identified; the remaining ticks were stored at –80 C and examined for zoonotic pathogens. Only adult *Hyalomma aegyptium* were found among the subsample of ticks collected for spur-thighed tortoise. The prevalence of tick infestation did not vary significantly within the study area but differences in intensity were observed in relation to the size of tortoises and the vegetation coverage. Our results provide strong evidence that adult *H. aegyptium* is the predominant tick species found on wild spur-thighed tortoises in northern Tunisia, where the species is commonly traded illegally across the Mediterranean Basin. Considering the potential transmission of several zoonotic pathogens by *H. aegyptium* to humans, we highlight the need to develop a surveillance system to prevent the introduction and the spread of tick-borne pathogens in the Mediterranean Basin

**Key Points:**

* Tortoises rescued from the illegal Mediterranean wildlife trade have been reported to be highly infested with *Hyalomma aegyptium*
	+ *H. aegyptium* is a hard-tick with a typical three-host life cycle
	+ Definitive host = Palearctic tortoises of genus *Testudo*
	+ However, larvae and nymphs feed on a wide range of hosts: tortoises, birds, lizards, small mammals, cattle, and humans
	+ Distribution is restricted to the Mediterranean bioregion
* High infection prevalence (~30%) of *H. aegyptium* with Crimean–Congo hemorrhagic fever virus has been reported in spur-thighed tortoises captured in Algeria and in Syria
* In this study, *H. aegyptium* prevalence was 91%, varying 82-100% by capture location
	+ No significant difference in prevalence within the humid and subhumid areas of Tunisia
* Positive correlation between infestation intensity and the age/size of tortoises
* The highest Infestation intensity was observed in forests with dense shrubs
* No significant difference in prevalence in male and female spur-thighed tortoises

**TLDR:** *H. aegyptium* is the primary tick of spur-thighed tortoises in Tunisia and is a potential vector for Crimean–Congo hemorrhagic fever virus and other vector-borne diseases

**Related Articles:** *None on the current ACZM reading list*

Bishop, R. P., Odongo, D. O., Dolan, T. T., Dolan, R. B., Skilton, R. A., & Sayer, P. D. (2019). Theileriosis in mountain bongo repatriated to Kenya: a clinical and molecular investigation. *Journal of Zoo and Wildlife Medicine*, *50*(2), 342-349.

Abstract: Mountain bongo (*Tragelaphus euryceros isaaci*) from Kenya were exported to zoological institutions in North America and Europe in the 1970s and 1980s. In the following 20–30 years bongo numbers declined in Kenya and the Mountain Bongo Repatriation Project was launched. This resulted in **18 adult bongo, descendants of the original translocated bongo, being repatriated from the United States to Kenya in 2004. These newly arrived bongo were inadvertently exposed to heavy tick infestation** on release in a conservancy on the slopes of Mount Kenya. Mortality and morbidity occurred during the third week after arrival. ***Theileria* sp. infection was apparent from the history, clinical signs, and necropsy findings, and *Theileria-*like parasites were detected microscopically in samples from sick and dead animals. Four bongo died before the outbreak was controlled.** In order to identify the *Theileria* parasite conclusively, molecular amplification techniques were used. A combination of reverse line blotting, with small subunit ribosomal RNA (SSU rRNA) polymerase chain reaction (PCR) amplification and nucleotide sequencing, identified the protozoan parasite ***Theileria taurotragi*,** suggesting this as the most probable cause of mortality and morbidity in the repatriated bongo.

**Key Points:**

* Eastern or mountain bongo – Threatened, rare antelope in Kenya.
	+ Kenya Bongo Surveillance Project, 100 total remain in wild.
	+ 1970s and 1980s, exported ~35 animals to the US for zoos.
	+ Successful reproduction and planned for repatriation to Kenya in 2003/2004.
	+ 18 of the bongo heavily infested with ticks, four died. CS – anorexia, lethargy, disorientation/blindness.
		- Necropsy – pulmonary edema, splenic enlargement, generalized lymphadenopathy, hemorrhages on heart and LN sections.
			* Theileria-like schizonts in lymphocytic cells.
	+ Used pyrethroid pour-on product flumethrin 1% aka Bayticol for control.
	+ Theileriocidal drug buparvaquone together with long-acting oxytetracycline IM resulted in good recovery for one individual, remained blind.
	+ Tick Rhipicephalus appendiculatus is a known vector of theileriosis. *T. parva, T. taurotragi*. *T. parva* has survived 1+yr in infected ticks. *T. taurotragi* that infected and killed these bongo considered nonpathogenic under normal circumstances of endemic stability, but lethan in an environment of endemic instability with stress.
		- *Theileria spp* infect bovidae, rhinocerotidae, cervidae.
		- *T. taurotragi* also infect cattle, potentially wide host range.

**Conclusion:**

* *Theileria taurotragi* most probably cause of mortality in population of repatriated bongo in Kenya.

Elliott, J. A., Dickson, C. C., Kantar, L., O'Neal, M. R., Lichtenwalner, A., Bryant, A., ... & Kamath, P. L. (2021). Prevalence and Risk Factors of Anaplasma Infections in Eastern Moose (Alces alces americana) and Winter Ticks (Dermacentor albipictus) in Maine, USA. *The Journal of Wildlife Diseases*, *57*(4), 844-855.

Abstract: Eastern moose (Alces alces americana) are heavily parasitized by winter ticks (Dermacentor albipictus), the dominant cause of increased calf mortality in the northeastern US. Although much work has focused on the direct negative effects of winter tick on moose, it remains unknown whether diseases transmitted by ticks may also affect moose health or pose a risk to other species. We explored the role that moose and winter ticks play in transmission of the tick-borne bacterial pathogens, Anaplasma spp., which cause mild to severe illness in humans and domestic animals. Our objectives were to 1) estimate the prevalence of Anaplasma spp. in moose and winter ticks; 2) determine the phylogenetic placement of these strains with respect to those found in other hosts and vectors; and 3) explore risk factors of Anaplasma infection in moose. A total of 157 moose (142 calves, 15 adults) were captured in western (n=83) and northern (n=74) Maine in 2017 and 2018. We screened for Anaplasma spp. in moose whole blood samples using a genus-specific PCR assay targeting the 16S rRNA gene. Over half (54%) of the moose were infected with Anaplasma bacteria, with a greater proportion of moose harboring Anaplasma-infections in the western (67%) versus northern study areas (38%). Male moose exhibited a higher prevalence than did females (63% vs. 47%). In contrast, Anaplasma spp. prevalence in winter ticks was low (<1%). Sequencing and phylogenetic analysis revealed that the single Anaplasma strain in moose was highly divergent from the strain in winter ticks and most closely related to an uncharacterized North American cervid strain. We conclude that winter ticks are unlikely to play a significant role in Anaplasma transmission to moose; however, high infection prevalence warrants further investigation into the impacts of Anaplasma spp. infection on moose health.

**Introduction:**

* *Anaplasma* spp. - obligate intracellular rickettsial species that infect host blood cells
	+ *A. phagocytophilum* - human granulocytic anaplasmosis, *Ixodes scapularis* tick vector, fever, headache myalgia, malaise, leukopenia, thrombocytopenia, mild hepatic injury
		- Wildlife hosts: white-footed mouse, raccoon, gray squirrel, white-tailed deer, Eurasian moose (up to 82% prevalence)
		- Replicate within ticks or mechanical transmission (biting flies, fomites)
			* Transplacental reported in livestock
	+ *A. marginale* - bovine anaplasmosis, anemia, weight loss, death, or life-long chronic infx
* Winter tick (*Dermacentor albipictus*): primary ectoparasite of moose, primary cause of moose calf mortality in NE US
	+ Competent vectors of *A. marginale* experimentally but one-host, 1 year life cycle thought to limit vector transmission

**M+M:**

* Screened for Anaplasma spp. in moose whole blood samples using a genus-specific PCR assay targeting the 16S rRNA gene

**Results/Discussion:**

* 54% of moose positive on PCR: males > females, western > northern sites (lower density but poorer habitat in western, also less snow cover)
	+ Moose strains were uncharacterized but most closely related to cervid strains (esp WTD and mule deer) and distant common ancestor to *A. marginale, centrale, ovis*
* No winter ticks from *Anaplasma* positive moose were positive, only 1 winter tick sample was positive (0.41% prevalence) with a strain closest to *A. phagocytophilum* strain from Canada

**Conclusions:**

* Majority of moose in Maine are infected with an uncharacterized strain of *Anaplasma*, highly divergent from strains identified in their ectoparasites (winter and black-legged ticks)
* Winter ticks are an unlikely vector for *Anaplasma* in Eastern moose
* No evidence that moose are hosts of *A. phagocytophilum* in Maine (in contrast to European moose populations)



Milnes, E. L., Thornton, G. L., Delnatte, P., Léveillé, A. N., Barta, J. R., Smith, D. A., & Nemeth, N. M. (2019). Molecular detection of Babesia Odocoilei in wild, farmed, and zoo cervids in Ontario, Canada. *Journal of wildlife diseases*, *55*(2), 335-342.

Abstract: **Babesia odocoilei, a tick-borne protozoan hemoparasite of white-tailed deer (Odocoileus virginianus), is being increasingly recognized as a cause of disease in captive cervids in North America**. Historically **endemic in white-tailed deer**, the natural wildlife reservoir in the southeastern US, B. odocoilei has been recently **associated with hemolytic anemia in captive Eurasian tundra reindeer** (Rangifer tarandus tarandus), **wapiti** (Cervus canadensis), and **woodland caribou** (Rangifer tarandus caribou) in the northcentral and northeastern US and several Canadian provinces. The emergence of B. odocoilei is likely related to the northward expansion of the range of the **tick vector, Ixodes scapularis**, and possibly to cervid translocations. Following a disease outbreak in reindeer and wapiti at the Toronto Zoo in Ontario, Canada, we utilized a **prospective postmortem survey to investigate the prevalence of B. odocoilei in wild, farmed, and zoo cervids in Ontario** (n = 270) in 2016–18 by **PCR and DNA sequencing of spleen samples**. Zoo bovids have been suggested as potential hosts of B. odocoilei in zoos affected by cervid babesiosis, so we also collected postmortem samples from **five species of bovids** (n = 7) at the Toronto Zoo that died or were euthanized during this time. We detected B. odocoilei in 1% (2/142) of farmed red deer (Cervus elaphus) as well as in 3% (1/29) of captive wapiti and 4% (3/68) of wild white-tailed deer. **Tissues from all zoo bovids and caribou, zoo and wild moose (Alces alces), and farmed white-tailed deer, wapiti-red deer hybrids, and fallow deer (Dama dama), tested negative for B. odocoilei**. No clinical cases of babesiosis were encountered during this study. These findings suggest that **white-tailed deer are a potential natural wildlife reservoir for B. odocoilei in Ontario** and that **red deer and wapiti could serve as more-localized reservoirs**.

Key Points:

* All sequenced samples 100% identical to each other and to B. odocoilei isolates from host species and geographic locations
	+ Partial 18S rDNA sequence isolated from a fatal case of babesiosis in a Toronto Zoo reindeer in 2012 also identical
	+ Comparison of nuclear 18S rDNA sequences → accepted as a method for resolving questions of relatedness of Babesia spp. Isolates
* Life cycle: Gametogony in tick gut → gametes fuse → form a zygote → develops into kinete → invades and replicates in tick hemolymph → Sporogony: kinetes invade tick salivary glands
* Transmission: Susceptible cervids exposed by bite of infected tick that introduces infective stages into blood → invade erythrocytes → merogony via binary fission → infected erythrocytes rupture → merozoites invade new erythrocytes → either become trophozoites that undergo merogony again by binary fission or develop into nondividing gamonts that are infective to a tick when it feeds on cervid intermediate host
	+ Merogonic  stages on blood smear = single, paired, or tetrad pyriform and ring-shaped organisms, (usually in accolé position at periphery of erythrocyte)
* Maintenance of B. odocoilei within an ecosystem dependent both on I. scapularis as the definitive host and a mammalian intermediate host
* Subclinical B. odocoilei infection identified in endemic and exotic ruminants in Bovidae
	+ Markhor (Capra falconeri), zoo yak, wild bighorn sheep (Oviscanadensis nelsoni) in US

Takeaways: Babesiosis is an emerging Canadian disease, I. scapularis is vector and needs mammalian IH (likely all cervid spp, white-tailed deer most common). WTD established wildlife reservoir. Babesia odocoilei life cycle above. PCR sensitive for subclinical infections.



**Coyotes (Canis latrans) in Arizona, USA, exhibit immune and genetic evidence of rickettsial infections.**

Green EN, Porter WT, Howard AL, Yaglom H, Benford R, Busch JD, Nieto NC.

The Journal of Wildlife Diseases. 2020;56(2):261-269.

Rocky Mountain spotted fever (RMSF), caused by the bacterium Rickettsia rickettsii, was recognized as endemic in Arizona, US after a 2002 outbreak and has since been a public health concern. The brown dog tick (Rhipicephalus sanguineus sensu lato) is the principal vector of this pathogen in Arizona. Domesticated dogs (Canis lupus familiaris) are the tick's main host, so free-roaming dogs in peridomestic areas have been named the primary risk factor for human cases of RMSF. However, the sudden emergence and long-distance dispersal of the pathogen have not been adequately explained, and one possible mechanism could include wildlife. Coyotes (Canis latrans) are wide ranging in Arizona and closely related to dogs, so it is possible that brown dog ticks parasitize coyotes and infect them. Although R. rickettsii is the most severe spotted fever group (SFG) rickettsial pathogen in humans, others occur in Arizona, and antibodies raised against them are cross-reactive, so we more-broadly hypothesized that coyotes in Arizona are exposed to SFG rickettsiae. **We collected coyote tissues in spring 2016 and 2017. We tested sera for antibodies to R. rickettsii** and found 9% (8/**94**) of samples were antibody-positive with titers of ≥256. S**ubsequent quantitative PCR analyses of skin** showed evidence for Rickettsia spp. in 2.9% (4/**138**) of samples. These data suggest that coyotes have a role in the maintenance of SFG rickettsiae in Arizona. Further investigation is warranted to reveal which specific pathogen-vector complexes act on coyotes in the region and whether they represent a risk to human health.

**Background**

* Rocky Mountain Spotted Fever - *Rickettsia rickettsii*, tick-borne bacteria
	+ 4 antigenic-determinant groups: spotted fever group (*R. rickettsii*), typhus group (*R. typhi*), transitional group (*R. felis*), ancestral group (*R. bellini*)
* Transmitted by all life stages of several species of hard-bodied ticks
	+ Brown dog tick (*Rhipicephalus sanguineus*) is principle vector in AZ
	+ Dogs are considered sentinels for RMSF, Ab found in coyotes

**Key Points**

* No ticks found in 2 years of sampling coyote carcasses
* Overall 34% seroprevalence on IFA, no difference in year, sex, or age class
	+ 9% at higher titer cutoff
* 4/138 samples positive on pan-rickettsia qPCR of ear skin biopsies

**Conclusions**

* Coyotes in Arizona are exposed to spotted fever group rickettsia and it’s likely endemic

**Tick paralysis in a free-ranging bobcat (Lynx rufus).**

Persky ME, Jafarey YS, Christoff SE, Maddox DD, Stowell SA, Norton TM.

Journal of the American Veterinary Medical Association. 2020;256(3):362-4.

CASE DESCRIPTION **A free-ranging male bobcat (Lynx rufus) was evaluated because of signs of pelvic limb paralysis.**

CLINICAL FINDINGS Physical examination of the anesthetized animal revealed tick infestation, normal mentation, and a lack of evidence of traumatic injuries. Radiography revealed no clinically relevant abnormalities. Hematologic analysis results were generally unremarkable, and serologic tests for exposure to feline coronavirus, FeLV, FIV, and Toxoplasma gondii were negative. Results of PCR assays for flea- and common tick-borne organisms other than Bartonella clarridgeiae were negative.

TREATMENT AND OUTCOME **Ticks were manually removed, and the patient received supportive care and fipronil treatment**. **The bobcat made a full recovery within 72 hours after treatment for ticks, and a presumptive diagnosis of tick paralysis was made.** Identified tick species included Dermacenter variabilis, Amblyomma americanum, and Ixodes scapularis.

CLINICAL RELEVANCE To the authors’ knowledge, tick paralysis has not previously been reported in felids outside Australia. This disease should be considered a differential diagnosis in felids, including exotic cats, with signs of neuromuscular disease of unknown etiopathogenesis.

**Case report**

* ~15 month old free ranging MI bobcat (Lynx rufuus) presented for pelvic limb paralysis, diagnosed tick paralysis based on high tick parasitism and exclusion of other causes
	+ Treated with methylprednisolone, LRS, ccfa, ivermectin, buprenorphine, fipronil and tick removal
* Identified tick species included *Dermacenter variabilis*, *Amblyomma americanum*, and *Ixodes scapularis*
* First report of tick paralysis in a felid outside of Australia

**Background**

* Tick Paralysis: neurotoxin in the salivary glands of the tick blocks the release of transmitters from motor nerve terminals, resulting in a flaccid paralysis that is frequently first observed as hind limb incoordination
* Other possible clinical signs: mydriasis, vomiting, regurgitation, dysphonia, hypotonus, and dysfunction of the urinary bladder
* Treatment: tick removal, supportive care, tick antitoxin serum
* Many cases full recovery in 24-72hr
* Commonly diagnosed in domestic felids in AU infested with *Ixodes holocyclus* and *I. conuatus*

**Pathology and discrete typing unit associations of Trypanosoma cruzi infection in coyotes (Canis latrans) and raccoons (Procyon lotor) of Texas, USA.**

Hodo, C. L., Bañuelos, R. M., Edwards, E. E., Wozniak, E. J., & Hamer, S. A.

Journal of Wildlife Diseases 2020;56(1):134-144.

*Trypanosoma cruzi* is a vector-borne, protozoal parasite of mammals. Infected humans, dogs (*Canis lupus familiaris*), and nonhuman primates may remain asymptomatic or may develop Chagas disease, most commonly characterized by lymphoplasmacytic myocarditis with myocardial degeneration and fibrosis, ultimately resulting in heart failure. Although wildlife species have important roles as sylvatic reservoirs, investigations into the pathology of *T. cruzi* in wildlife are limited to a few studies documenting histologic lesions in opossums (*Didelphis* spp.) and raccoons (*Procyon lotor*). Pathology in coyotes (*Canis latrans*) has not, to our knowledge, been described, despite their recognition as a reservoir and close genetic relationship to domestic dogs. **Our objectives were to perform a detailed, comparative cardiac pathology study of sympatric, naturally infected coyotes and raccoons, to characterize the overall *T. cruzi* infection prevalence in the heart and blood of each species via PCR, and to identify infecting discrete typing units (DTUs). We sampled hunter-harvested coyotes (*n*=120) and raccoons (*n*=24) in a 28 county region of central and south Texas, US**. **Raccoons** were significantly more likely to have positive PCR results (*P*<0.001) with a prevalence of 62% (15/**24**), comprising DTU TcIV exclusively, with mild to no evidence of cardiac pathology. In contrast, **coyotes** had a lower infection prevalence (8%, 10/**120**), comprising DTU TcI exclusively, with lymphoplasmacytic myocarditis observed in four of the six PCR-positive animals. Many raccoons had PCR-positive blood and heart tissue simultaneously, supporting previous reports that raccoons maintain parasitemia into chronic stages of infection; in contrast, none of the PCR-positive coyotes were positive in both heart and blood. Our findings demonstrate marked differences in *T. cruzi* infection dynamics between coyotes and raccoons, with important implications for reservoir potential and their role in transmission cycles.

**Background**

* *Trypanosoma cruzi* - vector-borne agent of Chagas disease, ZOONOTIC, increasing threat in S US
	+ Multiplies in hindgut of triatomine insects, pass infectious trypomastigotes in feces
* Humans, dogs, and NHP may develop cardiac disease with sudden death or CHF
* More than 30 wildlife species are susceptible hosts in the US
	+ Likely route of transmission in raccoons and coyotes is ingestion of infected kissing bugs
* Seven discrete typing units TeI-TeVI associated with different geographical regions, mammalian hosts, and vector species; evidence for varying clinical outcomes in humans and dogs
	+ TeI and TeIV predominate in the US: opossums - TeI; skunks and woodrats - TeI, TeIV
* Other ddx for lymphoplasmacytic myocarditis in these spp: *Bartonella* (more commonly valvular endocarditis) and *Borrelia burgdorferi* (not common in TX)

**Key Points**

* 8% of coyotes, 62% of raccoons positive on PCR of whole blood or heart tissue
	+ Infected raccoons had a higher concentration of parasite DNA in blood than coyotes
* All coyotes were TeI only, all raccoons were TeIV only
* No intramyocellular *T. cruzi* amastigotes were observed in any sections of heart in either species
* Lymphoplasmacytic myocarditis was significantly associated with *T. cruzi* positive PCR in coyotes but not in raccoons (80% of positive raccoons had no significant inflammation in the heart)
	+ Also found *Hepatozoon americanum, Dirofilaria immitis,* and *Sarcocystis.*

**Conclusions**

* Both raccoons and coyotes were positive on *T. cruzi* PCR of blood and heart tissue so may be involved in the sylvatic transmission cycle
* Overall prevalence was higher in raccoons with little associated pathology - TeIV is likely host adapted
* Coyotes had lower prevalence but more severe histo lesions and exclusively TeI DTU

Latas, Patricia, et al. "Argas (persicargas) giganteus soft tick infection with **rickettsia hoogstraali** and relapsing fever **borrelia** on wild avian species of the desert southwest, usa." *Journal of wildlife diseases* 56.1 (2020): 113-125.

**Abstract**:

Changing climatic conditions and the northward expansion of ticks and pathogens are of immense importance to human, animal, and environmental health assessment and risk management. From 2014 through 2015, a wildlife rehabilitation center in south-central Arizona, US noted soft ticks (Argasidae) infesting 23 birds, including Cooper’s Hawks (Accipiter cooperii), Gray Hawks (Buteo plagiatus), Harris’s Hawks (Parabuteo unicinctus), Red-tailed Hawks (Buteo jamaicensis), Great Horned Owls (Bubo virginianus), Common Ravens (Corvus corax), and a Greater Roadrunner (Geococcyx californianus), during the late summer seasonal rainy seasons. The parasites numbered in the hundreds on individual birds. Infested birds were moribund, obtunded, or paralyzed on presentation, with no prior histories of illness or evidence of trauma. Tick and avian blood samples were collected for vector-borne pathogen analysis focusing on the molecular detection of Rickettsia and Borrelia species. Ticks were identified as the neotropical species of soft tick, Argas (Persicargas) giganteus; their occurrence in the southern US on raptors represented an expansion of host range. Pathogen testing of ticks showed that 41% of 54 ticks were infected with Rickettsia hoogstraalii and 23% of 26 ticks were infected with a relapsing fever Borrelia; both agents are associated with uncertain health consequences. Among the blood samples, one was infected with the same Borrelia spp.; this Red-tailed Hawk also had Borrelia-positive ticks. With supportive therapy, the majority of birds, 74% (17/23), recovered and were released or permanent residents. The management of soft tick–infested birds and mitigation of future disease risk will require additional characterizations of these poorly studied soft ticks and their associated pathogens.

**Summary**:

* Tick and avian blood samples were collected for vector-borne pathogen analysis focusing on the molecular detection of Rickettsia and Borrelia species
* document wild bird infestations with large numbers of the soft tick Argus giganteus in which approximately one third of infested birds showed distal-to-proximal ascending paralysis and other infested birds were obtunded or dyspnea and inability to swallow
* low percentage of birds affected but morbidity via direct injury, blood loss, and immunological impact to the patients was severe
	+ tissue damage
	+ inflammation
	+ anemia
	+ paralysis
* A. giganteus difficult to remove manually and slow to die immediately from topical application of acaricides
* Treatment - critical supportive care, doxycycline treatment, and application of acaricides - contributed to recovery and eventual release of most of birds
* appeared that ticks were highly mobile and migrated to adjacent cages rapidly
* Pathogen testing of ticks showed that 41% of 54 ticks were infected with Rickettsia hoogstraalii and 23% of 26 ticks were infected with a relapsing fever Borrelia Rickettsia
* R hoogstraalii - spotted fever group rickettsia with unknown pathogenicity
* With supportive therapy, the majority of birds, 74% (17/23), recovered and were released or permanent residents
* several avian tick and blood samples associated with PCR amplicons and DNA sequences with imperfect matches to known relapsing fever Borrelia species in GenBank database

Currie, Chase R., et al. "Efficacy of white-tailed deer (Odocoileus virginianus) treatment for **cattle fever ticks** in Southern Texas, USA." *Journal of wildlife diseases* 56.3 (2020): 588-596

Abstract: **White-tailed deer (*Odocoileus virginianus*) serve as a host for cattle fever ticks (*Rhipicephalus* [*Boophilus*] *microplus* and *Rhipicephalus* [*Boophilus*] *annulatus*; CFTs); therefore, deer are a concern for CFT control programs in southern Texas, US.** Systemic (oral delivery of ivermectin) and topical (permethrin on pelage) treatment devices have been developed for white-tailed deer; however, the efficacy of these treatment options has not been determined for CFTs in southern Texas. **Our objectives were to evaluate the effectiveness of CFT treatment strategies by 1) measuring exposure rates of deer to the acaricides permethrin and ivermectin, 2) determining the relationship between CFTs on deer and exposure to the acaricides, and 3) determining if photos from remote cameras at medicated bait sites can be used as a measure of acaricide treatment.** We captured 327 deer at four sites in southern Texas. Deer visitation to medicated bait sites was monitored using remote cameras from March 2010 to February 2012. **There was no relationship between the presence of permethrin and the probability of being infested with CFTs (*P*≥0.336). The probability of infestation with CFTs decreased as serum ivermectin levels increased for male (*n*=18, *P*=0.098) and female (*n*=33, *P*<0.001) deer. Our results indicate ivermectin may be more effective in treating CFTs than permethrin;** thus it would be worthwhile to develop topical acaricides other than permethrin for treating white-tailed deer in southern Texas.

Key Points:

* Deer are involved in disease cycles as reservoirs for infectious agents or indirectly as reservoir hosts of tick vectors transmitting diseases to other animals and humans.
* Cattle fever ticks i.e. Rhipicephalus microplus and Rhipicaphalus annulatus.
	+ One-host ticks with a LC that includes an on-host and off-host phase.
	+ Cattle primary hosts, various life stages also found in WTD. Issue for eradication.
	+ CFTs are vectors for cattle fever (Babesia).
		- WTD not affected by Babesia bovis but support dispersal and maintenance of the CFT vectors.
* Deer in this area are treated with ivermectin-laced corn from Feb to July and a 4 Poster permethrin delivery system from Aug to January (topical; ivermectin cannot be fed during hunting season for risk of human consumption). Permethrin basically on paint rollers near feeding tubes at bait sites.
	+ Captured deer using a net gun fired from a helicopter.
	+ Tagged, rubbed with filter paper for detection of permethrin on pelage.
	+ Collected blood for ivermectin concentrations in serum.
	+ If one CFT found on a deer, considered infested.
	+ Monitored deer accessing bait sites with cameras over a two year period.
* CFT infestation rate of deer during year 1 was three times higher than year 2.
* Ivermectin levels were higher in serum captured in year 1 vs year 2.
* Greater proportion of males had permethrin on their skin in both years vs females.
* No statistical relationship between presence of permethrin and frequency of infestation with CFT.
* For all deer, frequency of deer with CFTs decreased with increased ivermectin levels.
* Presence of permethrin and serum ivermectin concentrations of individual deer were correlated with the number of photos with each deer, cameras were a good measure of deer visitation to bait sites and subsequent med exposure.
	+ Males – Presence of permethrin was more strongly correlated than ivermectin with photos.
	+ Females – Moderately strong correlation between the number of photos and either the presence of permethrin or serum ivermectin concentration.
	+ Relatively low proportion of fawns with ivermectin in serum and photographic data at bait sites, may be due to dominance hierarchies.

Takeaway: Ivermectin systemic tx may be more effective in decreasing CFTs on WTD vs permethrin topical treatments.

Medkour, Hacène, et al. "Molecular investigation of **vector-borne pathogens** in red foxes (Vulpes vulpes) from southern France." *Journal of wildlife diseases* 56.4 (2020): 837-850.

ABSTRACT: Because of their free-ranging nature, the probability of wild animals being exposed to vector-borne pathogens is likely higher than that of humans and pets. Recently, the red fox (*Vulpes vulpes)*has been suspected as being a reservoir or host of several pathogens of veterinary and public health importance. We conducted a molecular survey on 93 red foxes hunted in 2008–18, in the departments of Bouches-du-Rhone and Var, in southeastern France, for pathogens including *Leishmania infantum*, *Piroplasmida*, *Hepatozoon* spp., nematodes, *Coxiella burnetii*, *Borrelia* spp., *Rickettsia* spp., and *Anaplasmataceae*. **Spleen samples were screened for the presence of vector-borne pathogens** by PCR followed by sequencing. **Pathogens were detected in 94% (87/93) of red foxes**, and coinfections were identified in 24% (22/93) of foxes. We identified DNA from ***Hepatozoon canis, L. infantum, and Babesia vogeli*in 92% (86/93), 15% (14/93), and 3% (3/93) of red foxes, respectively**. We also found DNA of nematodes in 3% (3/93) of foxes; *Spirocerca vulpis* was identified in one fox and Dirofilaria immitis in the two others. Interestingly, ***C. burnetii* genotype 3, previously described in humans from the same region, was identified in 3% (3/93) of foxes** and *Anaplasma platys* in 2% (2/93) of foxes. We did not detect DNA of Borrelia spp., Bartonella spp., or Rickettsia spp. **In our study, the prevalence of pathogens did not vary by fox origin, sex, or tick carriage**. Molecular evidence of*B. vogeli, H. canis, S. vulpis, D. immitis, C. burnetii,* and *A. platys* in red foxes has not previously, to our knowledge, been reported from southern France. We propose that red foxes are potential reservoirs for several pathogens, including major zoonotic agents such as *L. infantum*. They could be incidental hosts for pathogens, such *C. burnetii*. The high prevalence for *H. canis* suggests an important role of foxes in domestic dog (*Canis lupus familiaris*) infection. These animals may pose a threat to human and animal health.

Key Points:

* In Europe, foxes are the most abundant wild carnivore. Main reservoir for rabies in western and central Europe.
* Assess the prevalence of vector borne diseases (*Leishmania infantum*, *Piroplasmida*, *Hepatozoon* spp., nematodes, *Coxiella burnetii*, *Borrelia* spp., *Rickettsia* spp., and *Anaplasmataceae*) in spleen samples via PCR.
* 10 years of samples collected from regulated hunting
* 94% of foxes infected with at least one pathogen
* 92% *Hepatozoon canis*
* Reservoir for domestic canids, transmitted by *Rhipicephalus sanguineus* tick.
* 15% *Leishmania infantum*
* Zoonotic – visceral and cutaneous forms in humans
* *Dirofilaria immitis*
* Two cases identified. Previous studies indicated higher prevalence in foxes from irrigated areas than semiarid regions.
* *Coxiella burnetii*
* Etiologic agent of Q fever (incidental hosts)
* Isolated same genotype that was found on a human heart valve from same region
* No difference in prevalence of infection based on origin, sex, or tick carriage.

Take home:

* Wild foxes sampled in Southern France had a high prevalence of vector borne disease, most commonly *Hepatozoon canis*, however other notable infections included *Leishmania infantum* (15% of cases), *dirofilatia immitis*, and *coxiella burnetii*.

**ANALYSIS OF PLASMODIUM LINEAGES IDENTIFIED IN CAPTIVE PENGUINS (SPHENISCIFORMES SPP.), EIDERS (SOMATERIA SPP.), AND INCA TERNS (LAROSTERNA INCA) IN A NORTH AMERICAN ZOOLOGICAL COLLECTION**

JZWM 51(1): 140–149, 2020

Natasha Spottiswoode, Susan L. Bartlett, Kenneth J. Conley, Tracie A. Seimon, Daniel O. Griffin, and John M. Sykes

Abstract: Vector-borne Plasmodium spp. infect a wide range of bird species. Although infections may be asymptomatic, certain genera, especially those that evolved in regions without endemic malaria, appear particularly susceptible to symptomatic disease, leading to morbidity and mortality. High mortalities associated with malaria infections have been documented in captive species of Sphenisciformes, Somateria, and Larosterna, all genera that evolved in climates with low mosquito exposure. To better characterize trends in Plasmodium-related mortality in a zoological collection in New York, necropsy reports for birds of all three genera that died between 1998 and February 2018 were analyzed; comparisons were made between birds that died with or without evidence of malaria infection. A seasonal peak in deaths was observed in birds regardless of their malaria status. There was no significant difference in the age of birds at death between malaria-positive and malaria-negative animals. These results suggest that age and season of death were not associated with malaria status. To investigate an association between parasite lineage and clinical outcome, polymerase chain reaction was used to identify parasite lineage in necropsied birds as well as healthy birds sampled as part of surveillance studies. Twelve different Plasmodium lineages were identified. The relative prevalence of parasite lineages was compared between necropsy and surveillance samples. A single parasite lineage, SGS1 (species: Plasmodium relictum), was significantly more likely to be found in surveillance samples; it was detected in a plurality of surveillance data but found in only one necropsy case. Other parasite lineages were more likely to be found in necropsies than in surveillance samples, most notably SEIAUR01 (species: Plasmodium cathemerium). These data may be consistent with a difference in virulence between parasite lineages. This investigation has implications for the monitoring and care of vulnerable avian species.

Introduction:

* Vulnerable species are those from naïve to plasmodium
* Humans: Prevalent species: *P. falciparum* (higher virulence), *P. vivas* (formant in liver, reactivates)
* Avian Plasmodium has exooerythorcitic tissue stages (phanerozoites), humans o not. Also, may affect various species
* Penguins: susceptible. Mortality recognized in Malgallenic (*S magellanicus*) and African (*S. demersus*)
* Historical detection: blood smears. Now – cytochrome b genes
	+ MalAvi- unified database for avian malaria cytochrome secuences = *P. relictum*
* Types of plasmodium: specialists- certain avian species; generalist – many species.
	+ *P. relictum, P elongatum* and P *cathemericum* are generalists.
* P. tejerai- caused mortality in penguins Magellanic penguins.
* P. elongatum – associated with mortality in penguins

Material and methods

* Inca terns (*Larosterna inca*), penguins (*Spenisciformes)* and eiders (*Somateria*) in outdoor exhibit in NY.
* Prophylaxis chloroquine phosphate or primaquine; juvenile inca- experimental treatment when young prior to fledging with monthly ponazuril.
* Postmortem cytology – lung, liver, and spleen.
* Positive malaria only when intraerythrocytic schizogonia was identify.
* PCR was performed if one of 3 conditions were fulfilled: if parasites detected on smears; clinical suspicion but no cytology performed or cytology was negative.
	+ Clinical suspicion: lethargy, inappetence, dyspnea during summer or early fall
* Recorded if < 1 yo, >1 yo, season
* Surveillance performed opportunistically

Results:

* Majority of mortalities noted in summer/early fall regardless of positive or negative results.
* Majority of mortality in eiders and inca terns were hatchlings. Juvenile birds are susceptible to Aspergillus particularly in their first summer.
* Plasmodium lineage SEIAUR01 – detected in liver. Lineage L1NN1 detected in spleen

Discussion:

* Predominance of SGS1 (*P. relictum*) in surveillance samples.  (Had cause mortality in Hawaiian avifauna)
	+ Documented in Europe and Africa. Only once in North and Sound America.
* SEIAUR01 more common on necropsy

**BLOOD PARASITE INFECTIONS IN STRIGIFORMES AND PSITTACIFORMES SPECIES IN CAPTIVITY WITH A NEW RECORD OF POTENTIAL FATAL BLOOD PARASITE TRANSMISSION TO PARROTS.**

JZWM 2021, *51*(4), 799-813.

Abstract: Although parrot species are infrequently infected by hemoparasites in the wild, some fatal infections have been reported in captive individuals. Conversely birds of prey are frequently infected by hemoparasites. In this study, 193 captive birds from Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) centers in Madrid, Spain, belonging to orders Psittaciformes, Accipitriformes, Strigiformes, and Falconiformes, were blood-sampled in search of parasite infections. Molecular and microscopic analyses were conducted to detect parasites of the following genera: *Haemoproteus*, *Plasmodium, Leucocytozoon*, *Trypanosoma*, *Babesia*, and *Lankesterella*. Infections by microfilariae and Coccidia were also searched in blood samples**. Surprisingly, infections by *Haemoproteus syrnii,* a common parasite from owls, were detected in the cadavers of two species of parrots, *Trichoglossus haematodus* and *Psittacula cyanocephala*. The same haplotype was also detected in the cadavers of two owl species, *Tyto alba* and *Strix rufipes*. All these birds were housed and died in the same center. Infections by species of *Plasmodium, Leucocytozoon,* and *Trypanosoma* were also found in different species of raptors. Nocturnal raptors (Strigiformes) show significantly higher prevalence of infection by blood parasites than diurnal raptors (Falconiformes and Accipitriformes). In conclusion, a potential fatal transmission of *Haemoproteus syrnii,* from Strigiformes to Psittaciformes species, is reported and several infections by different blood parasites were detected in birds of prey.** These results emphasize the importance of increasing prevention measures to avoid or reduce the transmission of blood parasites among birds from different species housed in these types of centers.

* Key Points:
	+ Most common hemoparasites in birds – Haemoproteus, Leucocytozoon, Plasmodium (Haemosporidia, Apixomplexa).
	+ Generally considered low pathogenicity but can cause mortality in juveniles and weakened individuals, contribute to population decline.
	+ Psittaciformes commonly infected.
		- Haemoproteus handai, H. psittaci, H. homohandai, Plasmodium dissanaikei.
	+ Birds of prey also commonly infected.
	+ Looked at live birds and cadavers, blood smears and PCR for Haemoproteus, Plasmodium, Leucocytozoon, Trypanosoma, Babesia, Lankesterella, microfilariae, Coccidia. Phylogenetic analysis.
	+ Prevalence in Psittaciformes spp significantly lower than raptors overall.
		- Hemoparasite infection found in 2 parrot cadavers: Trichoglossus haematodus and Psittacula cyanocephala
		- Haplotype detected corresponds to Haemoproteus syrnii which is frequently detected in STrigiformes.
		- Live individuals of Psittaciformes were not infected.
			* Proposed factors – Innate immunity, exclusive tropical distribution where prevalence of infection is low, long incubation periods, intake of vit B1, sampling methods that do not detect that tissues phases, absence of vectors, nest building behaviors in elevated locations with repellant plants.
	+ Prevalence in Strigiformes significantly higher than diurnal raptors.
		- Specifically Bubo capensis, Bubo bubo, Bubo bengalensis and a Bubo bubo x Bubo bengalensis hybrid.
	+ Haemoproteus parasites were the predominant parasites reported (9% prevalence) followed by Leucocytozoon, Trypanosoma, and Plasmodium.
	+ Babesia, Lankesterella, microfilariae, coccidia not detected.
	+ Phylogenetic analysis indicated that all haplotypes of hemoproteus and  FIEB-L3, FIEB-L4, FIEB-75 leucocytozoons were clustered within a monophyletic clade.
	+ Haplotype FIEB-H2 was found infecting only cadavers of Strigiformes and Psittaciformes.
	+ Leucocytozoon sequencing showed three haplotypes detected in Strigiformes that clustered with sequences detected in Columbiformes.
		- Leucocytozoon danilewskyi is the only spp of Leucocytozoon described for Strigiformes spp. Different haplotypes were detected.
	+ Plasmodium relictum historically described in Falconiformes and Psittaciformes, in this study only detected in Strigiformes.
		- 4 out of 21 infected individuals were negative by PCR and positive by microscopy.
		- 4 infections detected by PCR not seen on microscopy. Combo of techniques is ideal.
	+ Infected individuals could be a source of infection to other birds housed in the same facility.
		- Important to establish prevention measures to avoid or reduce hemoparasite transmission among birds in captivity.
			* Placement of mosquito nets in outdoor facilities, maintenance of animals in indoor facilities at least during the periods of higher activity fo vectors, or use of mosquito repellents and larvicides in facilities and their surroundings.
			* Routine veterinary evaluation of blood smears.
			* Treatment as needed with antimalarials.
* Takeaways: Psittacines housed with birds of prey are at risk for hemoparasite transmission.



**ASSESSMENT OF VARIATION IN THE DETECTION AND PREVALENCE OF BLOOD PARASITES AMONG SYMPATRICALLY BREEDING GEESE IN WESTERN ALASKA, USA**

JWD 2021 57(4), 799–807

Abstract: Haemosporidian parasites may impact avian health and are subject to shifts in distribution and abundance with changing ecologic conditions. Therefore, understanding variation in parasite prevalence is important for evaluating biologically meaningful changes in infection patterns and associated population level impacts. Previous research in western Alaska, US, indicated a possible increase in Leucocytozoon spp. infection between Emperor Geese (Anser canagicus) sampled in 1996 (,1%, n1⁄4134) and during 2011–12 (19.9%, 95% confidence interval [CI]: 3.0–36.8%, n1⁄477); however, different detection methods were used for these estimates. Prior research in this same region identified a lack of Leucocytozoon spp. parasites (0%, n1⁄4117) in sympatrically breeding Cackling Geese (Branta hutchinsii minima) in 2011. We molecularly screened blood samples collected from sympatrically breeding Emperor and Cackling Geese in western Alaska during additional breeding seasons to better assess temporal and species-specific variation in the prevalence of blood parasites. We found similar prevalence estimates for Leucocytozoon spp. parasites in Emperor Goose blood samples collected in 1998 and 2014, suggesting consistent infection of Emperor Geese with blood parasites at these time points. Using samples from sympatric geese sampled during 2014, we found evidence for a higher incidence of parasites among Emperor Geese (20.3%, 95% CI: 11.8–32.7%) compared to Cackling Geese (3.6%, 95% CI: 1.1–11.0%), reinforcing the previous finding of species-specific differences in infection. Furthermore, we detected Leucocytozoon, Haemoproteus, and Plasmodium spp. blood parasites in unflighted goslings of both species, supporting the possible transmission of these parasites at western Alaska breeding grounds. Our results help to clarify that prevalence of Leucocytozoon spp. parasites have probably remained consistent among Emperor Geese breeding in western Alaska since the late 1990s and that this species may disproportionally harbor Leucocytozoon spp. compared to sympatrically breeding Cackling Geese.

Summary:

* Intro:
	+ Common avian hemoparasites: Leucocytozoon, Haemoproteus, Plasmodium
		- Leucocytozoon spp. - transmitted by black flies
		- Haemoproteus spp. – transmitted by mosquitoes and biting midges
		- Plasmodium spp. – transmitted by mosquitoes
	+ Climate changes = alter the abundance of parasites 🡪 more likely to occur in high-latitude regions, where effects of climate change have been most pronounced
	+ Objective: assess detection and prevalence of avian haemosporidian parasites in Emperor and Cackling Geese breeding on the YKD, compared  1998 and 2014
* M+M:
	+ blood collected from Emperor Geese during incubation and brood rearing in 1998 and 2014, and from Cackling Geese during brood rearing in 2014, near Manokinak River
	+ tested for Leucocytozoon, Haemoproteus, or Plasmodium spp. using PCR
* Results/discussion
	+ all hemoparasites identifies in hatch year birds during brood drives but most were Leucocytozoon
	+ Emperor Geese have probably consistently harbored Leucocytozoon spp. infections through recent time
		- Prevalence ~20%
	+ sympatrically breeding Emperor Geese and Cackling Geese may differentially harbor Leucocytozoon spp. infections
		- prevalence of Leucocytozoon spp. in Emperor Geese estimated >5x that of Cackling Geese sampled on YKD, despite these species nesting and rearing broods in same geographic area
	+ hatch year geese on YKD may harbor a diversity of haemosporidian parasite infections that may not be as readily detected using PCR as they are in adult birds