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ABSTRACT BOOK



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test the possibility that polymicrobial infections exist in post-mortem brain tissue samples from patients with Alzheimer's disease using overlapping molecular methods. To establish a link between neurocognitive disorders and microbial or polymicrobial infections, autopsy samples will be examined with immunohistochemistry, highly sensitive polymerase chain reaction, and RNA in situ hybridization. The aforementioned methods were used to successfully detect *Borrelia burgdorferi*, *Bartonella henselae*, *Treponema denticola*, and *Candida albicans* in neural tissue. These findings further indicate that microbes should be considered in the etiology of neurocognitive disease. Though the etiopathogenesis of Alzheimer's disease remains controversial, this study seeks to better elucidate the multifactorial neuropathology associated with dementia-inducing disorders as well as provide compelling evidence for the existence of persistent infection in brain tissue.

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EXAMINING THE ROLE OF NYMPHAL IXODES IN THE TRANSMISSION OF BORRELIA BURGDORFERI TO DOGS

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In the United States, Lyme disease (LD) is the most commonly reported vector-borne disease among humans. LD is caused by *Borrelia burgdorferi* which is transmitted to mammals through the bite of infected Ixodes ticks. Nymphal Ixodes, which quest in late spring and early summer, are responsible for the majority of transmission to humans; adult ticks are responsible for a subtler peak of cases in the fall. *B. burgdorferi* seroprevalence among dogs has been used to estimate LD risk among humans; however, past research has suggested that dogs are less susceptible to infection from nymphal Ixodes, possibly indicating a different host preference between dogs and humans for these different life stages. To evaluate this, we reviewed LD serology results from serially tested dogs over a 9-month period to better understand timing of seroconversion and frequency of transmission by Ixodes nymphs versus adults ticks to canine hosts. In 2016, blood was collected from 215 dogs at 3 timepoints (February, August, and November). In February, blood was tested by SNAP 4Dx Plus Test and *Borrelia burgdorferi* C6 ELISA. Testing was limited to C6 ELISA for later timepoints. Dogs were considered serologically positive for LD if they were positive by SNAP 4Dx Plus Test or *Borrelia burgdorferi* C6 ELISA. Of 161 dogs serologically negative for *B. burgdorferi* in February, 4 seroconverted by August. All 4 dogs resided in the East region. Of 146 dogs that were serologically negative in August, 15 seroconverted by November; dogs resided in the East (10), Mid-west (3), South (1) and West (1) regions. Although the majority of canine incident cases as indicated via seroconversion occurred during adult tick season, results indicate that four dogs became infected prior to adult tick season. Future studies may be warranted to better understand the role of nymphal Ixodes ticks and *B. burgdorferi* transmission in dogs. Nymphal transmission of *B. burgdorferi* to dogs has important implications for dog-owners, veterinarians and researchers studying LD among dogs, especially in circumstances where dogs are used as proxies for human risk.

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MULTI-DRUG THERAPY IS REQUIRED TO EFFECTIVELY TREAT BARTONELLA INFECTION IN DIFFERENT ENVIRONMENTS

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Bartonella is a gram negative, facultative intracellular bacterium that manifests as different clinical syndromes collectively known as bartonellosis. The well-known diseases caused by these bacteria are cat scratch disease (*B. henselae*), trench fever (*B. quintana*) and Carrion's disease (*B. bacilliformis*). Excluding *B. bacilliformis*, which is evolutionarily more distinct than the 30+ other species, *Bartonella* infections result in self-limiting disease that is often undiagnosed and untreated. However, individuals with compromised immune systems may experience clinical

manifestations, which can become life threatening and need to be treated with effective antibiotics. To date, there is no standard treatment course for these infections and many doctors prescribe antibiotics based on limited case studies. It has been shown that *Bartonella* can grow extracellularly, intracellularly, and in biofilms. To determine an effective antibiotic strategy, it is important to understand *Bartonella* susceptibility in each of these growth conditions. We hypothesize that combination antibiotic treatments are required to effectively eliminate *B. quintana* and *B. henselae* growth, particularly in biofilm and intracellular environments. In previous studies, *B. henselae* treatment with single antibiotics in different media, as well as in DH82 canine macrophages, was ineffective in preventing growth. We plan to expand this work with different antibiotics supported by case reports, as well as double and triple combination therapy in erythrocytes and biofilms. Antibiotics tested were the following: doxycycline, gentamicin, azithromycin, azlocillin, rifampin, and clarithromycin. The effectiveness of combination therapy supports the notion that *Bartonella* species utilize target cells and biofilms as an antibiotic evasion strategy in the treatment of bartonellosis.

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DIVERSITY AND DNA BARCODING OF IXODIDAE AND ARGASIDAE TICKS IN THE US-MEXICO BORDER REGION OF THE MUNICIPALITY OF JUAREZ, CHIHUAHUA

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Ticks are the most important arachnids for human and animal health because they are vectors of a plethora of disease-causal agents, including bacteria and arboviruses. In the border municipality of Juárez, Chihuahua, severe cases of human rickettsiosis and a high prevalence of bacteria transmitted by ticks in domestic animals have been reported in recent years. Inadequate morphological identification due to similarity between morphospecies or identification of juvenile stages is a common problem of the prevention and control programs. As a result, DNA barcode technology is a reliable support tool for completing the morphological identification of ticks at the border between Mexico and the United States. This study reports the diversity and DNA barcode of Ixodidae (hard) and Argasidae (soft) ticks collected between 2018-2022 along this Mexican border municipality. Based on morphology and confirmed species identity using DNA barcoding, 3245 ticks belonging to four species were collected along Juárez municipality in Chihuahua, state. Ticks were identified as *Rhipicephalus sanguineus*, *Dermacentor albipictus*, *Otobius megnini*, and *Argas persicus*. A Bayesian analysis was constructed with a sample of 65 Cytochrome Oxidase subunit I mitochondrial sequences of the ticks collected. The topology of Bayesian tree displayed tree groups of *R. sanguineus*, whereas the clades of other species were well-defined. The Markov model of nucleotide substitution for distance estimation show a mean (\pm SE) of 18 (\pm 1.0) %. The intraspecific distance ranged between 0 to 0.02 %, whereas the interspecific distance was reached 11.9 to 29.5 %. Dogs were the major host of *Rh. sanguineus*, whereas *O. megnini* were predominant mostly on cows and horses. *A. persicus* were collected on soil, and *D. albipictus* were collected only on one deer. Finally, the public health importance of these species from the perspective of the public health of transboundary United States-Mexico region is also discussed.