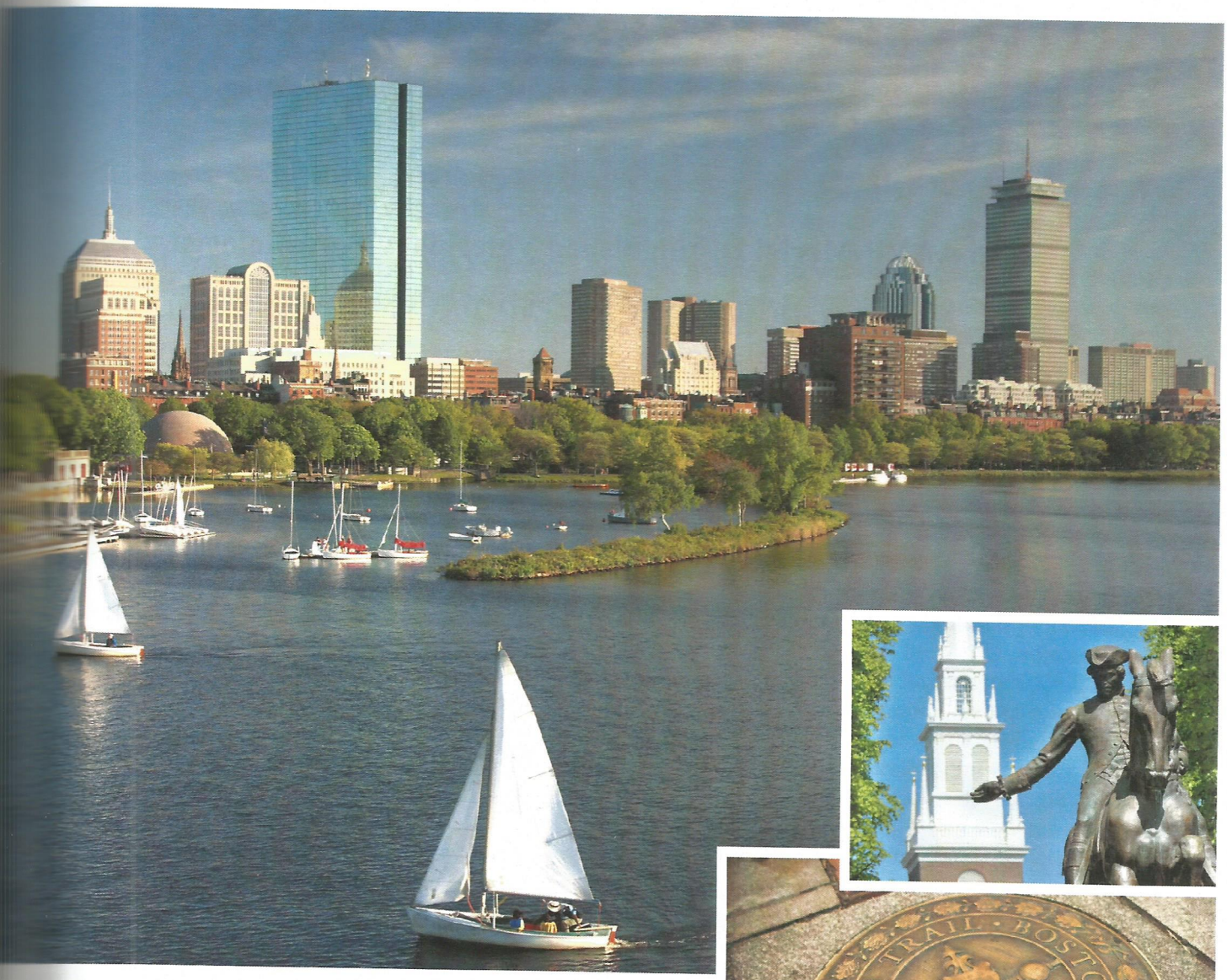

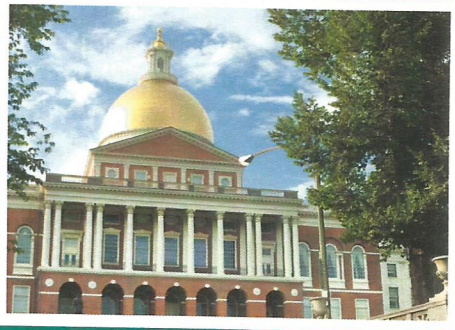

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increase with giardiasis. Dogs with giardiasis may initially be asymptomatic carriers, though they often develop tissue damage and gastrointestinal symptoms over time. It is unknown if fecal lactoferrin is elevated in canine giardiasis.

Aim: Evaluate fecal lactoferrin concentrations in dogs with giardiasis compared to healthy cohorts.

Methods: *Giardia* status was determined by Zinc Sulfate and Immunofluorescence Assay. The patient cohort was comprised of dogs from shelters/rescues, wellness visits, and screenings of recent diarrheal illness. Healthy cohorts included asymptomatic *Giardia*-infected and uninfected dogs. Stool consistency was ranked 1-5 from liquid to formed consistency. Canine fecal lactoferrin concentrations were evaluated using an enzyme-linked immunosorbant assay (ELISA).

Results: In this study, 98 canine fecal specimens were included from 3 veterinary laboratories in Oklahoma (68.4%), Colorado (18.4%), and Virginia (13.3%). The male to female ratio was 1:1, with 57 *Giardia*-infected dogs. Median fecal lactoferrin concentrations were significantly higher ($p<0.0001$) in *Giardia*-infected dogs (8.51µg/mL) than in uninfected dogs (0.00µg/mL). *Giardia* cyst count had no correlation to lactoferrin concentration, though cyst count ($p=0.0012$) and lactoferrin levels ($p=0.0018$) were significantly different in the formed-stool consistency group. When comparing clinical presentation, *Giardia* cyst count was significantly higher in recent diarrheal dogs than in wellness visit dogs ($p=0.0067$). Lactoferrin levels trended higher for dogs with recent diarrhea compared to healthy dogs, independent of *Giardia* status.

Conclusion: Our findings show that lactoferrin concentrations are significantly higher in dogs with giardiasis than in their healthy cohorts. Lactoferrin concentrations and *Giardia* cyst count were significantly lower in the formed-stool consistency group. Additional studies are needed comparing fecal lactoferrin to endoscopy and histology for assessing mucosal inflammation.

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Molecular Detection of Pathogens in *Rhipicephalus microplus* Populations from Veracruz, México.

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Bovine babesiosis, caused by several species of *Babesia* including *B. bigemina*, and anaplasmosis, caused by *Anaplasma marginale*, are tick-borne diseases affecting cattle wherever in the world the tick vector *Rhipicephalusmicroplus* is endemic. The detection and control of these pathogens are required to protect animal health problems and to mitigate the economic impact caused by them. The objective of this study was to investigate the presence of *A. marginale* and *B. bigemina* genetic material in *R. microplus* ticks from different properties in Mexico. Forty-one *R. microplus* tick samples were collected in 7 different Mexican farms. DNA was extracted using

a protocol containing guanidine thiocyanate and phenol. DNA quality was evaluated using spectrophotometry. A polymerase chain reaction (PCR) assay was applied for pathogen detection using specific primers for *B. bigemina* amplifying a 262 base pairs fragments (bp), and for *A. marginale*, generating a 458 bp amplicon. PCR products were separated by agarose gel electrophoresis and visualized with ultraviolet light for photographic records. Preliminary results are presented here. Two samples were positive for *A. marginale*, which were collected in the same farm (PZTM), and one sample was positive for *B. bigemina* (Tres Hermanos). The use of PCR for diagnosing these diseases offers enhanced and faster sensitivity and specificity on current infectious process as compared to serological tests. These aspects also offer the opportunity to understand co-infection status and the implications for the clinician trying to deal with the effects of tick-borne diseases on animal health and production.

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Diversity of the brown dog tick, *Rhipicephalus sanguineus,* in North America.

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The brown dog tick, *Rhipicephalus sanguineus,* has a worldwide distribution due to the ubiquity of its primary host, the domestic dog. However, different populations of *R. sanguineus* vary in their behavior and ability to transmit different disease agents. Recent review of morphology and mitochondrial gene sequences of brown dog ticks collected from Europe, Asia, South America, and Oceania has shown that the *R. sanguineus* complex parasitizing dogs is actually comprised of several distinct taxonomic units commonly referred to as *R. sanguineus* sensu lato, *R.* sp. I, *R.* sp. II, and *R.* sp. III. To determine the genetic diversity of *R. sanguineus* in the United States and the Caribbean, we examined ticks collected from several geographic locations (n=10), including Oklahoma, Texas, Illinois, Florida, and Haiti. All ticks were identified as brown dog ticks by morphologic examination and comparison to standard keys. Ticks were also dissected and mitochondrial 12s genes amplified and sequenced. To date, sequence analysis has confirmed the presence of both *Rhipicephalus* sp. II (southern lineage) and *R. sanguineus* sensu lato (northern lineage), suggesting multiple morphotypes are present in the region. Analysis of additional brown dog tick specimens from North America will allow more complete understanding of the full extent of diversity in the *R. sanguineus* complex and likely has important implications for disease transmission, including zoonotic risk.

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Identification of *Ixodes scapularis* tick saliva proteins sequentially injected into host every 24 hours through five days of feeding.

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Ticks are blood-feeding ectoparasites that surpass all arthropods in transmission of a greater variety of pathogens. Tick saliva is known to contain a mixture of pharmacological active components: proteins and other molecules that facilitate blood meal uptake and disease agent transmission by ticks. Majority of the individual key components utilized by the tick are unknown. In this study we conducted a comprehensive time-course feeding study to identify 582 tick and 82