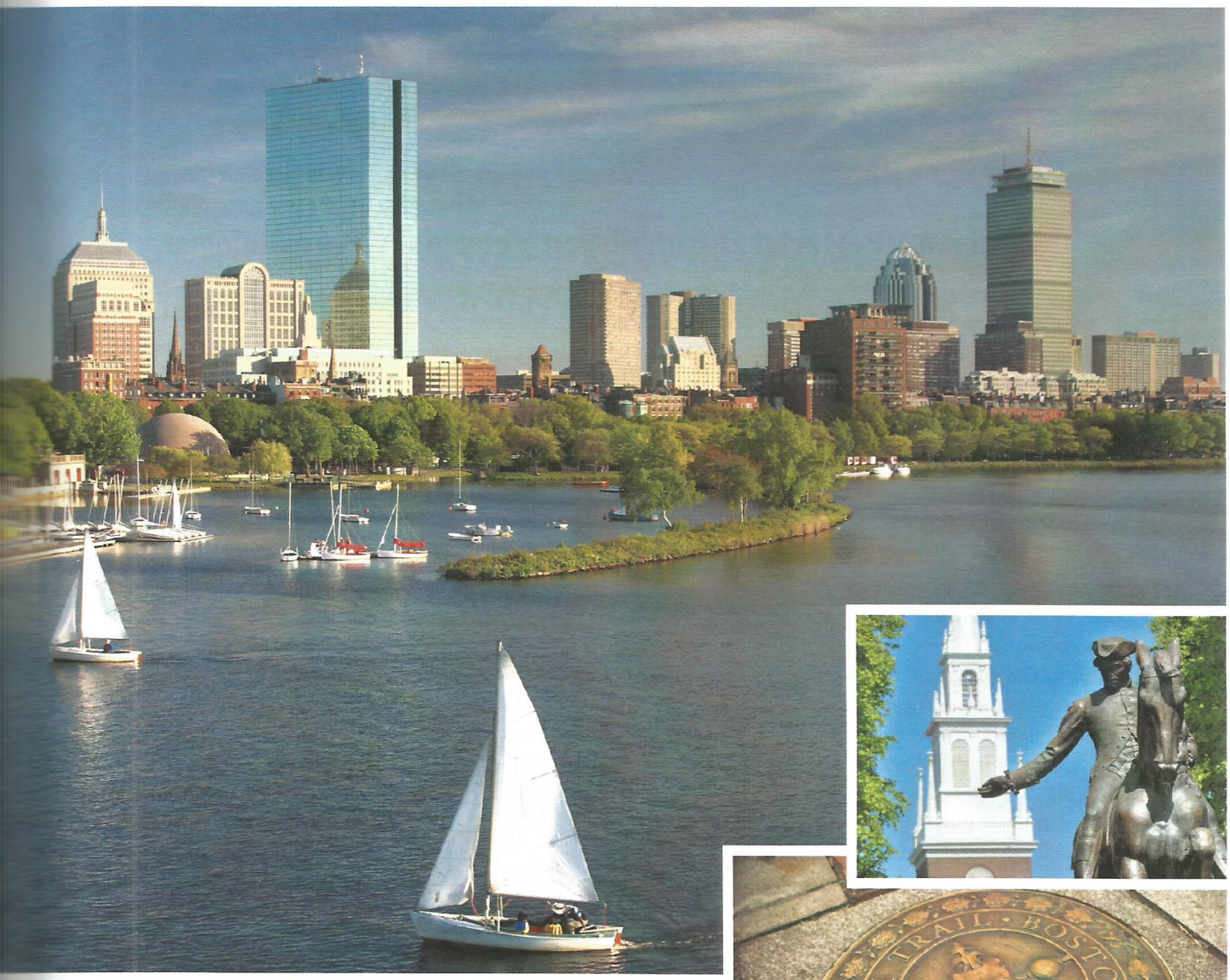

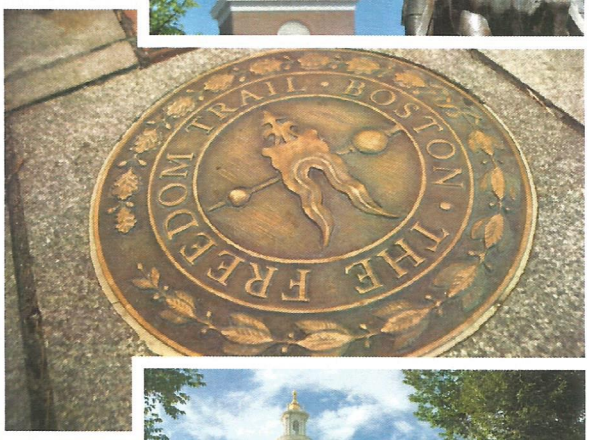

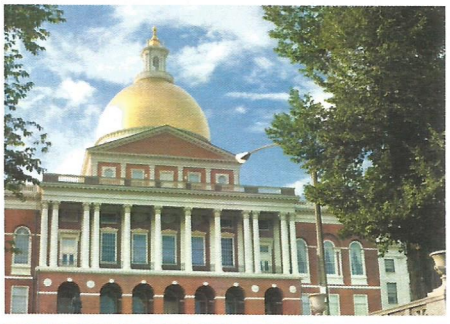

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host derived proteins in *Ixodes scapularis* tick saliva during feeding. We used a systems biology approach to identify proteins in *I. scapularis* tick saliva every 24h through the first five days of feeding. We have also identified proteins in saliva of ticks that were engorged and about detach from the host, as well as engorged and spontaneously detached. Tick and host derived proteins identified here are categorized based on biological function. Protein categories include proteinase, proteinase inhibitor, glycine rich proteins, immunity, lipocalin, heme/iron metabolism, secreted conserved protein, metabolism (amino acid, carbohydrate, energy, intermediate, lipid, nucleotide), and nuclear regulation. Others are classified as cytoskeletal, extracellular matrix/ cell adhesion, oxidant metabolism/ detoxification, proteasome machinery, protein export machinery, protein modification machinery, signal transduction (including apoptosis), transcription machinery, transporter/ receptors, and unknown protein families. T- and/or Z-score analysis of spectral counts show relative abundance of each protein class throughout the tick feeding process. The novel catalog of *I. scapularis* tick saliva proteins identified in this study provides an in depth view at protein families and/or molecular systems that are present at the *I. scapularis* tick and host interface every 24h. These data provides a foundation for in depth tick feeding physiology studies.

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Phylogenetic and phylogeographic relations of *Rhipicephalus microplus* (Acari: Ixodidae) in Brazil.

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The tick's large genetic diversity and expansion process need new studies that relate the genetic mutations. When ticks develop genetic variability, due to mutations, this may influence tick resistance to acaricides and efficacy of new vaccines. The objective of this work was to perform phylogenetic and phylogeographic relations inference on ticks from five different Brazilian regions, which were identified molecular analysis as *Rhipicephalus microplus*, using molecular marker cytochrome oxidase gene, subunit 1 (COX-1) and internal transcript spacer 2 gene, (ITS2). Fragments with (643 bp) for COX-1 and (580 bp) for ITS2 from 22 sample corresponding to the five Brazilian regions, were obtained. These results showed the cryptic complex in the *R. microplus* population from Brazilian regions. Value with FST (0.80212) suggests high signals of structuration, the values presented in this study strongly suggest that America clusters represent different species compared to Asia clusters. The common signal of high haplotypic diversity and low nucleotide diversity given by COX-1 and ITS2 genes was shared for the five Brazilian regions analyzed. These values are characteristic of a population that are in process of expansion and was corroborated with the negative values of the neutrality tests and the start structure of the haplotype networks. It is possible to conclude that samples from COX-1 tree has strong support for monophyly of the *R. microplus* Brazilian complex and are distinct from other populations all over the world. The genetic variability presented by the markers may influence tick resistance to acaricides and the attempt to develop new vaccines against this parasite, contributing to the transmission of new pathogens.