Abstract

Ticks are blood-feeding arthropods and serve as a vector and reservoir for diverse microbial pathogens of medical importance. Recent environmental and socio-economic changes have supported the invasion and expansion of ticks into new geographical areas, prompting a public health alert as ticks can transmit multiple pathogens during blood-feeding and cause polymicrobial infections with debilitating clinical outcomes. Thus, it is critical to closely monitor changes in local tick populations and educate clinicians about established and emerging tick-borne pathogens and associated diseases. This information will assist clinicians in making early diagnoses and prompt treatments to prevent severe clinical outcomes. The Long Island (NY) ecosystem is known to support diverse mammalian host species that have contributed to the establishment of three tick species: Amblyomma americanum, Ixodes scapularis, and Dermacentor variabilis. Our recent longitudinal tick survey discovered that an exotic tick species, Haemaphysalis longicornis, has successfully expanded in Long Island. Among them, A. americanum is the most abundant tick species with aggressive biting behavior, transmitting multiple pathogens, including Rickettsia amblyommatis (mild spotted fever rickettsiosis) and Ehrlichia (ehrlichiosis), and causing alphagal syndrome (red meat allergy). I. scapularis transmits multiple pathogens, such as Borrelia burgdorferi (Lyme disease), Babesia microti (babesiosis), and Powassan virus (neuroinvasive encephalitis). Although ticks carry multiple pathogens, there exists a significant gap in knowledge on tick-borne polymicrobial infections. To elucidate these shortcomings, this application aims to 1) document longitudinal tick population changes and their impacts on tick-borne diseases in Long Island, 2) determine the biological impacts of polymicrobial infections in ticks and mammalian hosts, and 3) characterize acute and convalescent host responses in patients exposed to tickborne pathogens. The proposed application integrates ecological and clinical approaches with molecular tools, addresses unexplored features of tick-borne diseases, and establishes a strong foundation for the upcoming program project application (P01, NIAID, PAR-22-225).