



## V 20 Endemic, newly invaded, and cryptic cycles – Lyme borreliosis emergence in the Upper Midwestern United States

Sarah A. Hamer<sup>a,b</sup>, Jennifer L. Sidge<sup>b</sup>, Michelle E. Rosen<sup>a</sup>, Edward D. Walker<sup>c</sup>,  
Graham J. Hickling<sup>d</sup>, Jean I. Tsao<sup>a</sup>

<sup>a</sup> Dept. of Fisheries and Wildlife, Michigan State University, East Lansing, Michigan, U.S.A.

<sup>b</sup> College of Veterinary Medicine, Michigan State University, East Lansing, Michigan, U.S.A.

<sup>c</sup> Dept. Microbiology and Molecular Genetics, Michigan State University, East Lansing, Michigan, U.S.A.

<sup>d</sup> The Center for Wildlife Health, University of Tennessee, Knoxville, Tennessee, U.S.A.

Emergence of Lyme disease in the eastern US is linked to recent range expansion of the vector *Ixodes scapularis*, the blacklegged tick, which spreads the etiologic agent, *B. burgdorferi*. The question we pose is what might be the contribution of cryptic cycles to emergence of *B. burgdorferi*? One hypothesis is that expanding *I. scapularis* populations introduce *B. burgdorferi* into the naïve environment. Another non-mutually exclusive hypothesis is that *B. burgdorferi* already exists in these environments, in cryptic cycles involving vectors that feed on wildlife but not on humans. Invading *I. scapularis* might thus acquire *B. burgdorferi* by feeding on hosts shared by cryptic-cycle ticks.

To begin testing this hypothesis, we initiated complementary field studies. First, we surveyed for *B. burgdorferi* at sites where *I. scapularis* has not yet invaded. We detected low prevalences of *B. burgdorferi* in wildlife tissues and wildlife-associated ticks. Second, we assessed the prevalence and genetic diversity of *B. burgdorferi* in an *I. dentatus* rabbit–bird cycle at a site where *I. scapularis* has not yet invaded. At that site, 3.5% of birds carried *B. burgdorferi*-infected ticks with both novel and previously-identified genetic strains (suggesting gene flow with other *B. burgdorferi* populations). Third, we compared *B. burgdorferi* genetic diversity along a gradient of *I. scapularis* establishment. We found no structure in *B. burgdorferi* from adult ticks from 5 states spanning a 750-km, 30-year invasion pathway.

Together, these data suggest that cryptic vectors and vagile wildlife reservoirs contribute to the spread and emergence of *I. scapularis*-driven Lyme disease.