Population dynamics of the Lyme disease bacterium, *Borrelia burgdorferi*, during rapid range expansion in New York State

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Abstract

Recent changes in climate and human land-use have resulted in alterations of the geographic range of many species, including human pathogens. Geographic range expansion and population growth of human pathogens increase human disease risk. Relatively little empirical work has investigated the impact of range changes on within-population variability, a contributor to both colonization success and adaptive potential, during the precise time in which populations are colonized. This is likely due to the difficulties of collecting appropriate natural samples during the dynamic phase of migration and colonization. We systematically collected blacklegged ticks (*Ixodes scapularis*) across New York State (NY), USA, between 2006 and 2019, a time period coinciding with a rapid range expansion of ticks and their associated pathogens including *Borrelia burgdorferi*, the etiological agent of Lyme disease. These samples provide a unique opportunity to investigate the genetic dynamics of human pathogens as they expand into novel territory. We observed that founder effects were short-lived, as gene flow from long-established populations brought almost all *B. burgdorferi* lineages to newly colonized populations within just a few years of colonization. By seven years post-colonization, *B. burgdorferi* lineage frequency distributions were indistinguishable from long-established sites, indicating that local *B. burgdorferi* populations experience similar selective pressures despite geographic separation. The *B. burgdorferi* lineage dynamics elucidate the processes underlying the range expansion and demonstrate that migration into, and selection within, newly colonized sites operate on different time scales.

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