



Ecological Variables of Genetic Diversity in *Borrelia burgdorferi*, the Lyme Disease Bacterium

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Gould Seminar Room, (Rm 235) Gould Building (Bldg. 116), Linnaeus Way, ANU



Lyme disease is the leading reported vector-borne disease in the United States and continues to spread through the Northeast and Midwest. It is caused by *Borrelia burgdorferi*, a bacterium that circulates among vertebrate host species and is transmitted among hosts by the black-legged tick (*Ixodes scapularis*). The bacterium has high genetic variation at the outer surface protein C (*ospC*) locus, and past studies suggest that hosts act as ecological niches to the *ospC* genotypes. Five genotypes are known to be human invasive (HIS), making it crucial to examine disease risk at the genotypic level. My dissertation was focused on understanding the ecological drivers of *ospC* diversity and frequency profile at the

species, community, and landscape scales. I found that variation among nine host species and their associated *ospC* genotype frequency profiles suggest support for the ecological niche hypothesis. Short-tailed shrews (*Blarina brevicauda*) and American robins (*Turdus migratorius*) have high proportions of HIS to non-HIS genotypes, which suggests that they may contribute to higher disease risk. No significant trade-off was detected between occurrence frequency and transmission efficiencies of *ospC* types from ticks feeding on the host individuals. At the community level, host composition, but not necessarily host diversity, was an important predictor of *ospC* diversity and HIS infection prevalence. However, the extent to which these predictors influence *ospC* diversity and HIS infection prevalence was subject to annual and site variation. Obtaining better inclusive host community composition and diversity estimates could help with the predictive powers of these metrics on the *ospC* frequency profile, especially with HIS types. Lastly, landscape analysis showed that endemic areas of New York State have higher *ospC* richness and diversity than newly invaded areas, that there is high turnover of genotypes along the invasion scale, and that HIS types are relatively common across the landscape. This research sheds new light on the role of host composition and diversity in disease risk at the genotypic level, thereby expanding our knowledge of important host reservoirs of *B. burgdorferi*, and providing insights to the spread of Lyme disease in New York State.

Presented by

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