Selective Whole Genome Amplification (SWGA). Detecting finescale processes using population genetics and coalescent analyses is limited by the amount of available sequence data per sample (**Box 1**). For example, we and others have shown that *B. burgdorferi* MLST analyses resolves evolutionary and biogeographic patterns at continent-wide and millennial time scales[e.g. 34–37]. Phylodynamic analyses of several *B. burgdorferi* genes from the Hudson Valley, in contrast to our analyses of tick genes, had insufficient sequence variability to identify phylodynamic patterns at scales of 100's of kilometers and 10's of years. The genetic variation to overcome this limitation is found at the genomic scale[45–48]. **Genome sequencing will enable fundamental and previously unobtainable insights into fine-scale population processes**. Although sequencing small microbial genomes is inexpensive, obtaining sufficiently pure microbial DNA for next-generation sequencing requires laboratory culture, which is not feasible from frozen samples[49]. Thus, we pioneered the culture-free selective whole genome amplification technique to rapidly and cheaply amplify the genomes of only the target species from total genomic extracts of a tick (**C.3**[49–52]). We can obtain genome sequences from each microbial species in each sample, regardless of the number of microbial species in the sample. We anticipate that the 1,000's of genomes generated by this project will be applicable to address far more hypotheses than we will pursue, thus stimulating research across fields.

BOX 1: Phylodynamics: Evolutionary and ecological dynamics of pathogens have traditionally been studied through labor-intensive sampling of natural reservoirs and vectors. Phylodynamic analyses, which apply a coalescent framework to randomly sampled genetic sequences, are emerging as a powerful alternative for studying evolutionary and ecological dynamics. Phylodynamic analyses of viral systems - where mutations in genes and transmission events occur on similar time scales - have identified genes under selection for virulence, characterized population structure and migration routes, identified mutations leading to epidemics, and characterized evolutionary processes[43,53–58]. Similarly imperative insights into the ecological and evolutionary dynamics of cellular microbes - where transmission events and mutations across genomes occur on similar time scales - are feasible through phylodynamic analyses of genomes. Population genomic studies of microbial pathogens in nature provide exciting new prospects to identify ecological determinants of contemporary transmission processes and establish crucial links between disease risk and environmental variability.

Rigorous compilation of methods to accurately estimate demographic histories of multiple pathogens. We propose to couple advanced methodologies including serial-coalescent modeling, landscape genetics, and geospatial modeling to assess the demographic history of each microbial species. Each method is well established in our labs, but to our knowledge this combination of methods has only been used to accurately identify environmental factors that affect evolutionary and ecological dynamics of *I. scapularis* (**Fig. 2** and **3**[18,21–23,59]). We have shown that this integrative approach accurately links environmental factors to demographic patterns.

Experimental validation of phylodynamic models. Creating accurate models of environmental impacts on pathogen demography (**Aims 1** and **2**) will allow for robust estimates of 'real' areas that may be colonized in the future. We propose to assess the accuracy of model estimates using empirical samples collected from areas that are currently beyond the established geographic ranges of some, or all, of these species (**Fig. 1**). Many previous studies have estimated future growth or spread of organisms, but few have attempted to validate these estimates[16,60–64]. Although empirical model validation of highly variable ecological processes is challenging, our models of tick demography were highly accurate (**C.2**). Model validation is feasible in this system because the demographic dynamics of these pathogens appear to change at rates amenable to a five-year study (**Fig. 1**). Validated demographic models will be immediately useful in forecasting the spread of these pathogens, and subsequent disease risk.

(c) Research Strategy

We utilize multiple analytical approaches with data that span timeframes and geographies in which populations were changing in both size and geographic range. We have demonstrated that these approaches can delineate demographic patterns **and** identify the environmental