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Quantitative Vector Ecology: Modeling Tick-Borne Disease Risk in an Ecological Context

Vector-borne diseases are complicated because in addition to their impacts on human health, the pathogens responsible for disease are often dependent on complex enzootic cycles that may include many animal species and have specific environmental conditions. Tick-borne illnesses such as Rocky Mountain spotted fever (*Rickettsia rickettsii*), Tidewater spotted fever (*Rickettsia parkeri*), and Lyme disease (*Borrelia burgdorferi*), have significant public health implications, but the dynamics of these diseases cannot be understood or modeled without an understanding of the underlying ecology of the ticks and their hosts. Here we discuss the findings of our long-term field collection effort that brings together information on tick species, tick abundance, disease prevalence, and host and habitat preference over four years in the southeastern United States. Using our field data, we have created an agent-based model using Netlogo software. This model is designed to explore the dynamics of Gulf Coast ticks (*Amblyomma maculatum*) and prevalence of Tidewater Spotted Fever as these ticks are introduced into new geographic areas. We will compare the results of our model with discovery of a newly established population of Gulf Coast ticks, and we will discuss the proposed expansion of our model to include successional dynamics and additional tick and pathogen species.